

STIC-Biotech/ChemLib

89049

From: Bunner, Bridget
Sent: Friday, March 14, 2003 8:01 AM
To: STIC-Biotech/ChemLib
Subject: sequence search

Hi! I'd like to request a sequence search for case 09/686,020:

1. the amino acid sequence of SEQ ID NO: 2

Thanks!

Bridget Bunner

Art Unit 1647
CM1-10D12
(703) 305-7148
mailbox 10B19

Point of Contact:
Beverly Shears
Technical Info. Specialist
CM1 1E05 Tel: 308-4994

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Searcher: _____
Phone: _____
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TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
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Litigation: _____
Full text: _____
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Other: _____

VENDOR/COST (where applic.)
STN: _____
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24

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 03-17-03
Searcher: Beverly e 49914
Terminal time: 20
Elapsed time: _____
CPU time: _____
Total time: 23
Number of Searches: _____
Number of Databases: 1

Search Site

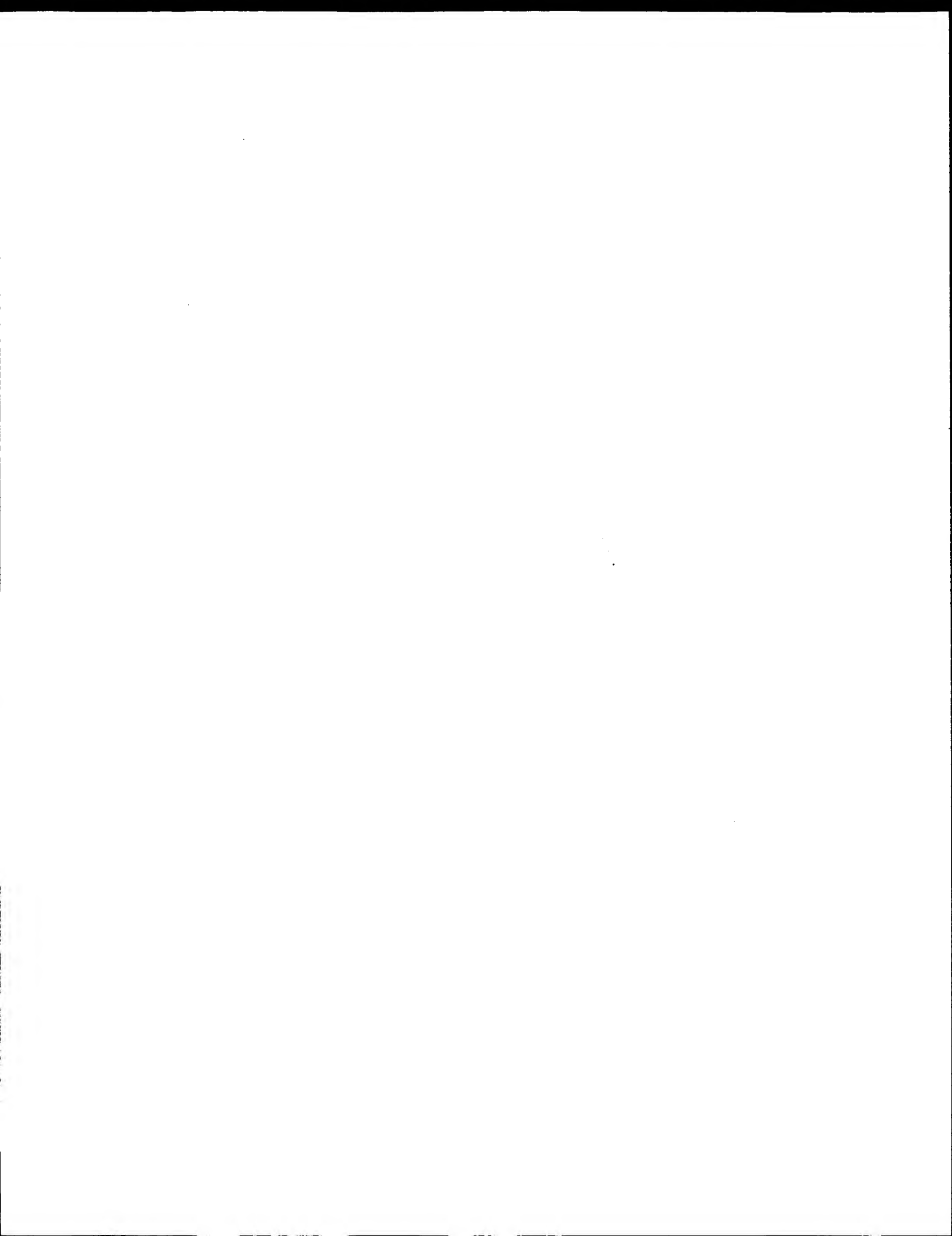
_____ STIC
_____ CM-1
_____ Pre-S

Type of Search

_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors

_____ IG Suite
_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
✓ _____ Other CGN



GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 16:07:45 ; Search time 11 Seconds
(without alignments)
1319.701 Million cell updates/sec

Title: US-09-686-020A-2

Perfect score: 1819

Sequence: 1 MALEQNGSTYYEENEMNG.....VEEPPDSGPTSTFSL 350

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database : SwissProt.40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query % | Match Length | ID | Description |
|------------|-------|---------|--------------|---------------|--------------------|
| 1 | 1819 | 100.0 | 350 | 1 CCR6_HUMAN | Q9NPB9 homo sapien |
| 2 | 1620 | 89.1 | 350 | 1 CCR6_BOVIN | P35350 bos taurus |
| 3 | 659 | 36.2 | 378 | 1 CCR7_HUMAN | P32248 homo sapien |
| 4 | 650 | 35.7 | 378 | 1 CCR7_MOUSE | P47774 mus musculu |
| 5 | 639 | 35.1 | 369 | 1 CCR9_MOUSE | Q9WU77 mus musculu |
| 6 | 637 | 35.0 | 357 | 1 CCR9_HUMAN | P51686 homo sapien |
| 7 | 605 | 33.3 | 367 | 1 CCR6_MOUSE | O54689 mus musculu |
| 8 | 583 | 32.1 | 374 | 1 CCR6_HUMAN | P51684 homo sapien |
| 9 | 581 | 31.9 | 342 | 1 CCR6_CERAE | O18983 cercopithe |
| 10 | 571 | 31.4 | 343 | 1 CCR6_MACMU | Q9X145 macaca mula |
| 11 | 569 | 31.3 | 342 | 1 CCR6_MACNE | O19024 macaca neme |
| 12 | 560 | 30.8 | 342 | 1 CCR6_HUMAN | P00574 homo sapien |
| 13 | 537.5 | 29.5 | 360 | 1 CCR4_HUMAN | P51679 homo sapien |
| 14 | 534.5 | 29.4 | 360 | 1 IL8B_HUMAN | P25025 homo sapien |
| 15 | 529.5 | 29.1 | 353 | 1 IL8B_PANTAR | Q28807 pan troglod |
| 16 | 527 | 29.0 | 384 | 1 CCR6_HUMAN | O00590 homo sapien |
| 17 | 525 | 28.9 | 362 | 1 CCR4_HUMAN | P46092 homo sapien |
| 18 | 524 | 28.8 | 362 | 1 CCR4_HUMAN | P54111 ratius norv |
| 19 | 522.5 | 28.7 | 353 | 1 IL8B_GORGO | Q28422 gorilla gor |
| 20 | 522.5 | 28.7 | 355 | 1 CCR4_HUMAN | P49238 homo sapien |
| 21 | 522.5 | 28.7 | 353 | 1 CCR4_MOUSE | P51680 mus musculu |
| 22 | 521.5 | 28.7 | 353 | 1 IL8B_MACMU | Q28519 macaca mula |
| 23 | 520.5 | 28.6 | 362 | 1 CCR4_MOUSE | O91121 mus musculu |
| 24 | 512 | 28.1 | 356 | 1 IL8B_MOUSE | O97571 canis fami |
| 25 | 511 | 28.1 | 354 | 1 CCR4_MOUSE | Q92049 mus musculu |
| 26 | 511 | 28.1 | 358 | 1 IL8B_RABIT | P35344 mus musculu |
| 27 | 504 | 27.7 | 360 | 1 CCR2_MACMU | O18793 macaca mula |
| 28 | 501.5 | 27.6 | 355 | 1 IL8A_RABIT | P11109 oryctolagus |
| 29 | 501.5 | 27.6 | 358 | 1 CCR3_CAVO | O92213 cavia porce |
| 30 | 500.5 | 27.5 | 352 | 1 CCR4_HUMAN | P30991 homo sapien |
| 31 | 499.5 | 27.5 | 353 | 1 CCR4_BOVIN | P25930 bos taurus |
| 32 | 499.5 | 27.5 | 360 | 1 IL8B_BOVIN | Q28003 bos taurus |
| 33 | 498.5 | 27.4 | 352 | 1 CCR4_PAPAN | P56491 papio anubi |

| | | | | | |
|----|-------|------|-----|--------------|--------------------|
| 34 | 498.5 | 27.4 | 352 | 1 CCR5_CERTO | O62743 cercopithec |
| 35 | 498.5 | 27.4 | 353 | 1 CCR4_FELCA | P56498 felis silve |
| 36 | 497.5 | 27.4 | 350 | 1 IL8A_GORGO | P55919 gorilla gor |
| 37 | 495.5 | 27.2 | 352 | 1 CCR5_CERAE | P56493 cercopithe |
| 38 | 494.5 | 27.2 | 352 | 1 CCR4_CERTO | O62747 cercopithec |
| 39 | 493.5 | 27.1 | 352 | 1 CCR4_MACFA | Q28474 macaca fasc |
| 40 | 493.5 | 27.1 | 352 | 1 CCR4_MACMU | P79394 macaca mula |
| 41 | 492.5 | 27.1 | 359 | 1 CCR3_RAT | O54814 ratius norv |
| 42 | 492.5 | 27.1 | 359 | 1 IL8B_RAT | P35407 ratius norv |
| 43 | 491.5 | 27.0 | 352 | 1 CCR5_PAPHA | P56441 papio hamed |
| 44 | 491.5 | 27.0 | 352 | 1 CCR5_PYGRI | O97880 pygathrix b |
| 45 | 490.5 | 27.0 | 352 | 1 CCR5_MACMU | P79436 macaca mula |

ALIGNMENTS

RESULT 1
ID CCR6_HUMAN STANDARD: PRT: 350 AA.
AC Q9NPB9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 11 (C-C CCR-11) (CCR-11)
DE (Chemokine receptor-like 1) (CCR1L) (CCX CCR).
GN CCR1 OR CCR2 OR VSHK1.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20200450; PubMed=10734104;
RA Schweickart V.U., Epp A., Raport C.J., Gray P.W.;
RT "CCR1L is a functional receptor for the monocyte chemoattractant
protein family of chemokines.";
RT J. Biol. Chem. 275:9550-9556(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20171478; PubMed=10706668;
RA Gedling J., Dairaghi D.J., Wang Y., Hanley M., Talbot D., Miao Z.,
Schall T.J.;
RT "Cutting edge: Identification of a novel chemokine receptor that binds
dendritic cell- and T cell-active chemokines including ELC, SLC, and
TECK.";
RT J. Immunol. 164:2851-2856(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20231748; PubMed=10767544;
RA Khaja H., Wang G., Ng C.-T.L., Tucker J., Brown T., Shyamala V.;
RT "Cloning of CCR1L, an orphan seven transmembrane receptor related to
chemokine receptors, expressed abundantly in heart.";
RL Gene 246:225-238(2000).
CC - FUNCTION: RECEPTOR FOR SCYA2/MCP1, SCYA8/MCP2, SCYA13/MCP4,
SCYA19/MIP3B/ELC, SCYA21/SLC AND SCYA25/TECK.
CC - SUBCELLULAR LOCATION: Integral membrane protein.
CC - TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN HEART, LOWER
EXPRESSION IN LUNG, PANCREAS, SPLEEN, SMALL INTESTINE AND FETAL
TISSUES.
CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC EMBL: AF193507; AAF61299.1; -
CC EMBL: AF233281; AAF44751.1; -
CC EMBL: AF110640; AAF59827.1; -
DR

DR Genev; HGNC:1611; CCRL1.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; 1.
 DR PROSITE: PS50262; G_PROTEIN_RECPT_FL_2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein.
 KW DOMAIN 1 42
 FT TRANSMEM 43 63
 FT DOMAIN 64 87
 FT TRANSMEM 88 108
 FT DOMAIN 109 113
 FT TRANSMEM 114 134
 FT DOMAIN 135 154
 FT TRANSMEM 155 175
 FT DOMAIN 176 201
 FT TRANSMEM 202 222
 FT DOMAIN 223 240
 FT TRANSMEM 241 261
 FT DOMAIN 262 289
 FT TRANSMEM 290 310
 FT DOMAIN 311 350
 FT CARBOHYD 5 6
 FT CARBOHYD 19 19
 FT DISULFID 112 184
 SQ SEQUENCE 350 AA; 39913 MW; 8E26049D25757C8 CRC64;

Query Match Best Local Similarity 100.0%; Score 1819; DB 1; Length 350;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEONOSTDYEEENMGTYDYSOYELICIKEDVREFAKFLPVFLTVFVIGLAGNS 60
 DB 1 MALEONOSTDYEEENMGTYDYSOYELICIKEDVREFAKFLPVFLTVFVIGLAGNS 60
 QY 61 MVAIAIAYKKKQRTKTDYIILNLAVALDLFTLPFMAVNAVHGVNLGKIMCKITTSALYT 120
 DB 61 MVAIAIAYKKKQRTKTDYIILNLAVALDLFTLPFMAVNAVHGVNLGKIMCKITTSALYT 120
 QY 121 LNFVSGMOFLACISIDRYAVATKVPSSGVGKPCMIICFCVMAAAILSTIPOLVFTVND 180
 DB 121 LNFVSGMOFLACISIDRYAVATKVPSSGVGKPCMIICFCVMAAAILSTIPOLVFTVND 180
 QY 121 LNFVSGMOFLACISIDRYAVATKVPSSGVGKPCMIICFCVMAAAILSTIPOLVFTVND 180
 DB 121 LNFVSGMOFLACISIDRYAVATKVPSSGVGKPCMIICFCVMAAAILSTIPOLVFTVND 180
 QY 181 NARCIPIFRYLGTSMKALIMLEICIGFVVPFLIMGVCFITARTLMKMPNKRISPLK 240
 DB 181 NARCIPIFRYLGTSMKALIMLEICIGFVVPFLIMGVCFITARTLMKMPNKRISPLK 240
 QY 241 VLTIVVIVETIYOLPYNIVKFCRAIDIIYLSITSCNMSKRDIAIOVTESIALPHSCLNP 300
 DB 241 VLTIVVIVETIYOLPYNIVKFCRAIDIIYLSITSCNMSKRDIAIOVTESIALPHSCLNP 300
 QY 301 ILVYFMGASFKNYMKYAKKGYSMRQROSVSEEPFDESGTEPTSTFESI 350
 DB 301 ILVYFMGASFKNYMKYAKKGYSMRQROSVSEEPFDESGTEPTSTFESI 350

RESULT 2
 CRRB_BOVIN
 ID CRRB_BOVIN STANDARD; PRT; 350 AA.
 AC P35350;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 11 (C-C CR-11) (CC-CR-11) (CCR-11)
 DE (Possible gustatory receptor type B) (PPR1 protein).
 GN CCRL1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_Taxid=9913;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Tongue; PubMed=8392843;
 RX MEDLINE=93326166; Aoki T., Kurihara K.;
 RA Matsuno I., Mori T.,
 RT "Identification of novel members of G-protein coupled receptor
 RT superfamily expressed in bovine taste tissue";
 RL Biochem Biophys. Res. Commun. 194:504-511(1993).
 CC SCVA19/MIPB/ELC, SCVA21/SIC, SCVA25/TECK (BY SIMILARITY).
 CC -1- FUNCTION: RECEPTOR FOR SCVA2/MCP1, SCVA25/TECK (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN CIRCUMVALLATE AND FUNGIFORM
 CC PAPILLAE, OLFACTORY EPITHELIUM AND LUNG. LOWER EXPRESSION IN
 CC LIVER, KIDNEY AND TONGUE EPITHELIUM BEARING NO TASTE PAPILLAE.
 CC VERY LOW EXPRESSION IN THE CEREBRAL CORTEX OF THE BRAIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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DR EMBL: S63848; AAB27547.1; -
 DR PIR: JN0621; JN0621.
 DR HSSP: P02699; 1BOJ.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; 1.
 DR PROSITE: PS50262; G_PROTEIN_RECPT_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Phosphorylation.
 KW DOMAIN 1 41
 FT TRANSMEM 42 66
 FT DOMAIN 67 79
 FT TRANSMEM 80 99
 FT DOMAIN 100 113
 FT TRANSMEM 114 135
 FT DOMAIN 136 153
 FT TRANSMEM 154 175
 FT DOMAIN 176 199
 FT TRANSMEM 200 222
 FT DOMAIN 223 241
 FT TRANSMEM 242 265
 FT DOMAIN 266 283
 FT TRANSMEM 284 306
 FT DOMAIN 307 350
 FT CARBOHYD 6 6
 FT CARBOHYD 19 19
 FT DISULFID 112 184
 SQ SEQUENCE 350 AA; 40008 MW; E46BF942F3919C82 CRC64;

Query Match Best Local Similarity 89.1%; Score 1620; DB 1; Length 350;
 Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

QY 1 MALEONOSTDYEEENMGTYDYSOYELICIKEDVREFAKFLPVFLTVFVIGLAGNS 60
 DB 1 MALEONOSTDYEEENMGTYDYSOYELICIKEDVREFAKFLPVFLTVFVIGLAGNS 60
 QY 61 MVAIAIAYKKKQRTKTDYIILNLAVALDLFTLPFMAVNAVHGVNLGKIMCKITTSALYT 120
 DB 61 MVAIAIAYKKKQRTKTDYIILNLAVALDLFTLPFMAVNAVHGVNLGKIMCKITTSALYT 120
 QY 121 LNFVSGMOFLACISIDRYAVATKVPSSGVGKPCMIICFCVMAAAILSTIPOLVFTVND 180
 DB 121 LNFVSGMOFLACISIDRYAVATKVPSSGVGKPCMIICFCVMAAAILSTIPOLVFTVND 180
 QY 121 LNFVSGMOFLACISIDRYAVATKVPSSGVGKPCMIICFCVMAAAILSTIPOLVFTVND 180
 DB 121 LNFVSGMOFLACISIDRYAVATKVPSSGVGKPCMIICFCVMAAAILSTIPOLVFTVND 180
 QY 181 NARCIPIFRYLGTSMKALIMLEICIGFVVPFLIMGVCFITARTLMKMPNKRISPLK 240
 DB 181 NARCIPIFRYLGTSMKALIMLEICIGFVVPFLIMGVCFITARTLMKMPNKRISPLK 240

| | |
|----|--|
| KM | G-protein coupled receptor; Transmembrane; Glycoprotein; Signal. |
| FT | SIGNAL |
| FT | CHAMIN |
| FT | DOMAIN |
| FT | TRANSSEM |
| FT | DOMAIN |
| FT | TRANSSEM |
| FT | DOMAIN |
| FT | TRANSSEM |
| FT | DOMAIN |
| FT | TRANSSEM |
| FT | DOMAIN |
| FT | TRANSSEM |
| FT | DOMAIN |
| FT | CARBOHYD |
| FT | DISULFID |
| FT | CONFLICT |
| FT | CONFLICT |
| SO | SEQUENCE |
| | 378 AA; 42874 MW; DACBA213841A1MB4 CXC64; |
| | Query Match |
| | Best Local Similarity 36.2%, Score 659, DB 1; Length 378; |
| | Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7; |
| OY | 1 MALPQNSTDYVEENEMNGTYDSQVELCIKEEDREFAKVFLPLFLTIVEIGLAGNS 60 |
| DB | 21 VCLCODEVTDDYIGNT---IVDTLFESLCSKRYRFRKAFELPIIMISILCFVLLGNG 77 |
| OY | 61 MVVAIYAAYKKORTKYDIYNLAVALDLLETPFPMAVNANVGWGLKIMCKITSALYT 120 |
| DB | 78 LVLTLYIEFKRKLTMTDYLLNLAAVDILLETLTFPMAYSAAKSVMFGVHCKLIIFATIK 137 |
| OY | 121 LNFVSGMGFLACTSIDRVAVATKVPSS---QSGVKPCMIICFCVMAAILSLPOLVFY 176 |
| DB | 138 MSFEFGMLLCISTIDRVAVAIQAASAHRRHRKRVLLISKLSGVGMILAIVSLIPELYS 197 |
| OY | 177 TVNDA-----RCPIPFPRYLGTSMKALIMLELICGEVNPFLANGCVFYTARTMKRP 231 |
| DB | 198 DLGRSSSQAMCSSLITEH--VENAFITTIQVANWIGFLVPLLANSPCYIVIIIRLLGAR 254 |
| OY | 232 NIKISRPLKVLTVTVIVETVOLPRNIYKFCADIIITSLITSCMSKRMDIAIOVYESI 291 |
| DB | 255 NEERKAARKVIIVAVVVEIVLPDPNGVLAQTVANFNITSSTCELSKOLNIAVDVTSYL 314 |
| OY | 292 ALFHSCLPNPIYVFMGASFKNYVMKVAKKG-----SW-----PRORSVEEPPFD 337 |
| DB | 315 ACVRCVCANPELFAFGVAFNRNDLKRLFDLGCLSEQDLROMSCHNIRRSSMSE----- 369 |
| OY | 338 SEGTEPTSTPS 349 |
| DB | 370 ---AETWTTFES 377 |
| | RESULT 4 |
| | CKR7_MOUSE |
| ID | CKR7_MOUSE STANDARD; PRT; 378 AA. |
| AC | P47774: |
| DT | 01-FEB-1996 (Rel. 33, Created) |
| DT | 01-FEB-1996 (Rel. 33, Last sequence update) |
| DT | 30-MAY-2000 (Rel. 39, Last annotation update) |
| DE | C-C chemokine receptor type 7 precursor (C-C CKR-7) (CC-CCR-7) (CCR-7) (MP-3 beta receptor) (EBV-induced G protein-coupled receptor 1) (EBI1). |
| GN | CCCR OR CMKBRT OR EBI1 OR EBI1H. |
| OS | Mus musculus (Mouse). |
| OC | Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. |
| OX | NCB1_Taxid=10090; |
| ON | [1] |

| | | | | | | |
|--------------|---|-----------|-----------------|------------|-----------------------------------|---|
| | FT | DOMAIN | 107 | 120 | EXTRACELLULAR (POTENTIAL). | . |
| | FT | TRANSSEM | 121 | 142 | CYTOPLASMIC (POTENTIAL). | . |
| | FT | DOMAIN | 143 | 160 | CYTOPLASMIC (POTENTIAL). | . |
| | FT | TRANSSEM | 161 | 181 | 4 (POTENTIAL). | . |
| | FT | DOMAIN | 182 | 210 | EXTRACELLULAR (POTENTIAL). | . |
| | FT | TRANSSEM | 211 | 238 | 5 (POTENTIAL). | . |
| | FT | DOMAIN | 239 | 254 | CYTOPLASMIC (POTENTIAL). | . |
| | FT | TRANSSEM | 255 | 280 | 6 (POTENTIAL). | . |
| | FT | DOMAIN | 281 | 304 | EXTRACELLULAR (POTENTIAL). | . |
| | FT | TRANSSEM | 305 | 322 | 7 (POTENTIAL). | . |
| | FT | DOMAIN | 323 | 369 | CYTOPLASMIC (POTENTIAL). | . |
| | FT | CARBOHYD | 32 | 32 | N-LINKED (GLCNAC. .) (POTENTIAL). | . |
| | FT | DISULFID | 119 | 198 | BY SIMILARITY. | . |
| SQ | SEQUENCE | AA: | 369 AA: | 41913 MM; | 6971F76FA24B4AE CRC64; | . |
| Query Match | Best Local Similarity | 35.1%; | Score 639; | DB 1; | Length 369; | . |
| Matches 118; | Conservative | 77; | Mismatches 111; | Indels 22; | Gaps 5 | . |
| OY | 10 DYYEENEMNGTY--DYSQYELCIKEDVREFAKVLPVLVEFYIAGLSNMYVAIV | 66 | : | : | : | : |
| Db | 16 DEFSDSTASDDYDMNLNFSSF--FCCKNVNRQFASHFLPRLYWLVEFGTIGNSLTVLY | 73 | : | : | : | : |
| OY | 67 AYYKKQETKRDVVYLMLAAVDLLLETPRPMVAVNHGVGKIMKTISTALTNVSG | 126 | : | : | : | : |
| Db | 74 WYCTRYATMTMDLMLNLADLFLELATLDEPMALAAAGMMQTOMTKVMSTKMNFYC | 133 | : | : | : | : |
| OY | 127 MQLPACTISDRYAAYATVKPVSGSVCPCW-----IIICVYMAAAILSPOLVFYT | 177 | : | : | : | : |
| Db | 134 VLIIMCISVDRIAYIVO-----AMKAQVWRQRKLRLYSKMCITILVMWAAYLCPEILDY | 188 | : | : | : | : |
| OY | 178 VNDN---ACRIPILPRPYLGTSMKALIQMLEICIGVVPFLMGICYFLTARTLMKMNIK | 234 | : | : | : | : |
| Db | 189 VSGEGTATCTMYPKDKNAKLKSALLKLVGLGFEPMAVCYTIILLHTLVQAOKSS | 248 | : | : | : | : |
| OY | 235 ISRELKTLVIVVFVTQLPYNIVYECRAIDIISLTCSNMSKRMEDIAIOVTESTIALF | 294 | : | : | : | : |
| Db | 249 KHKALKTITIVLVPFLMSQEPYNSILYQAVDAVAMFINSCTISINIDICQVGTIAIF | 308 | : | : | : | : |
| OY | 295 HSCINPLIYVFMGASFKNYVMKYAKYTG | 322 | : | : | : | : |
| Db | 309 HSCINPLIYVFMGASFKNYVMKYAKYTG | 336 | : | : | : | : |
| RESULT 6 | | | | | | |
| ID | CKR9_HUMAN | STANDARD; | PRT; | 357 AA. | | |
| AC | P51686; | | | | | |
| DT | 01-OCT-1996 (Rel. 34, Created) | | | | | |
| DT | 01-OCT-1996 (Rel. 34, Last sequence update) | | | | | |
| DT | 15-JUN-2002 (Rel. 41, last annotation update) | | | | | |
| DE | C-C chemokine receptor type 9 (C-C CKR-9) (CC-CKR-9) (CCR-9) (GPR-9- | | | | | |
| DE | 6). | | | | | |
| GN | CCR9 OR CMBR9. | | | | | |
| OS | Homo sapiens (Human). | | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | | | | |
| OX | NCBI_TaxID=9606; | | | | | |
| RN | [1] | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | |
| RA | Lautens L.L., Tiffany H.L., Gao J.-L., Modi W., Murphy P.M., | | | | | |
| RA | Bonner T.I.; | | | | | |
| RL | Submitted (APR-1996) to the EMBL/Genbank/DBJ databases. | | | | | |
| RN | [2] | | | | | |
| RP | CHARACTERIZATION. | | | | | |
| RX | MEDLINE=99248139; PubMed=10229797; | | | | | |
| RA | Zaballos A., Gutierrez J., Varona R., Ardauy C., Marquez G.; | | | | | |
| RT | "Identification of the orphan chemokine receptor GPR-9-6 as CCR9, the | | | | | |
| RT | receptor for the chemokine TECK." | | | | | |
| RL | J. Immunol. 162:5671-5675(1999). | | | | | |
| CC | -FUNCTION: Receptor for chemokine SCYA25/TECK. Subsequently | | | | | |
| CC | transduces a signal by increasing the intracellular calcium ions | | | | | |
| CC | level. Alternative coreceptor with CD4 for HIV-1 infection. | | | | | |

CKR6_MOUSE STANDARD; PRT; 367 AA.

AC 054689; 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE C-C chemokine receptor type 6 (C-C CKR-6) (CC-CKR-6) (CCR-6) (KYL11).

GN CCR6 OR CCR6B.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Yanagihara S., Komura E., Yamaguchi Y.;

RT "Mouse G protein-coupled receptor KRL11."

RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA MEDLINE=9077268; PubMed=9862452;

RA Varona R., Zaballios A., Gutierrez J., Martin P., Roncal F.,

RA Albar J.P., Ardavin C., Marquez G.;

RT "Molecular cloning, functional characterization and mRNA expression

RT analysis of the murine chemokine receptor CCR6 and its specific ligand

RT MIP-3alpha."

RL FEBS Lett. 440:188-194(1998).

CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-3-

CC ALPHA/LARC AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE

CC INTRACELLULAR CALCIUM IONS LEVEL.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

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CC or send an email to license@isb-sdb.ch).

CC -----

DR EMBL: AB009369; BAA23776.1; -

DR EMBL: AJ222714; CA10956.1; -

DR MGD: MG1:1333797; Cmkp6.

DR InterPro: IPR004067; CC_Chemokine6.

DR InterPro: IPR000276; GPCR_Rhodopsn.

DR Pfam: PF00001; 7tm_1; 1.

DR PRINTS: PRO1529; CHEMOKINER6.

DR PRINTS: PRO0237; GPCRHOOPS.

DR PROSITE: PS00237; G-PROTEIN RECP_F1.1; 1.

DR PROSITE: PS50262; G-PROTEIN RECP_F1.2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein.

FT DOMAIN 1 39

FT TRANSMEM 40 66

FT DOMAIN 67 75

FT TRANSMEM 76 96

FT DOMAIN 97 111

FT TRANSMEM 112 133

FT DOMAIN 134 151

FT TRANSMEM 152 172

FT DOMAIN 173 203

FT TRANSMEM 204 230

FT DOMAIN 231 246

FT TRANSMEM 247 271

FT TRANSMEM 272 295

FT DOMAIN 296 313

FT TRANSMEM 314 367

FT DISULFID 110 189

FT CARBOHYD 2 35

FT CARBOHYD 367 AA; 42102 MW; 6A309A83B1117E CRC64;

SO SQUENCE

Query Match 33.3%; Score 605; DB 1; Length 367;

Best Local Similarity 37.9%; Pred. No. 3e-30;

Matches 129; Conservative 60; Mismatches 125; Indels 26; Gaps 8;

QY 8 STDVYEEENMGNGTQDYSOYELI-----CIKEDYREFAKVLPVFLTVIVFYIGLAGNSM 61

DB 3 STEISYGTDD-----IDNTFYISIPDHGFCSLSEBRNFTKVFVPLAYSLICVYGLGIM 58

QY 62 VVAIYAVYKPKTKDVIYILNLAVALDLLFTLPMAV-NAVHGVLGKIMCKITSLALT 120

DB 59 VVMTFAFYKARKSMTDVYLLNMAIDILFVLTPMAVTHATNTVWFSDALCKIMKGYA 118

QY 121 LNFVSMQFLACISIDRYAVAVTKVPSQSGYKPC-----IICFCYMAAILSLPQVLF- 175

DB 119 VVNCGMILLACISMDRYAVIQAATKSRVRSRLTLTKHSKIVAWFISIISSPTFLN 178

QY 176 --YTVDNARCIPFPYRYLGTG---MKALIMLEICIGFVVPFLMGVCYFTARTLMK 229

DB 179 KYEELDRVC---EPRYSVSEPTWMLGMLGELFFGFTPLFMVFCYLFITKIVQ 235

QY 230 MPNIKISPLKVLTVIVVIVTOLPYNIVKFCRAIDIIYSLTSCNKRMDIAIOYTE 289

DB 236 AONSKRHRAIRVIAVIVLFLACQIPHNVLTVAVN-TGKVGRCSTEKVLAATRNVAE 294

QY 290 STALFHSCLNPLIYVEMGASFKNYMKVAKKGSRRQRO 329

DB 295 VLAFLHCLNPLVLAIFGQKERNYEMKIMKIDVWCRRKKNK 334

RESULT 8

CKR6_HUMAN STANDARD; PRT; 374 AA.

AC P51684; Q92846; P78533;

DT 01-OCT-1996 (Rel. 34, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE C-C chemokine receptor type 6 (C-C CKR-6) (CC-CKR-6) (CCR-6) (LARC

DE receptor) (GPR-CY4) (GPRCY4) (Chemokine receptor-like 3) (CCR-L3)

DE (DRY6).

GN CCR6 OR CCKBR6 OR STRL22 OR GPR29 OR CKRL3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A., AND FUNCTION.

RA MEDLINE=97313465; PubMed=9169459;

RA Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,

RA Nomiyama H., Yoshie O.;

RT "Identification of CCR6, the specific receptor for a novel

RT lymphocyte-directed CC chemokine LARC."

RL J. Biol. Chem. 272:14893-14898(1997).

RN [2]

RP SEQUENCE FROM N.A.

RA Laurens L.L., Modi W., Bonner T.I.;

RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA MEDLINE=97040707; PubMed=8886020;

RA Zaballios A., Varona R., Gutierrez J., Lind P., Marquez G.;

RT "Molecular cloning and RNA expression of two new human chemokine

RT receptor-like genes."

RL Biochem. Biophys. Res. Commun. 227:846-853(1996).

RN [4]

RP SEQUENCE FROM N.A.

RA McCoy R., Perlmutter D.H.;

RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.

RN [5]

RP SEQUENCE FROM N.A.

RA MEDLINE=97224503; PubMed=9070937;

RA Liao F., Lee H.-H., Farber J.M.;

RT "Cloning of STRL22, a new human gene encoding a G-protein-coupled

RT receptor related to chemokine receptors and located on chromosome

RT 6q27."

RL Genomics 40:175-180(1997).


```

FT TRANSMEM 188 215 5 (POTENTIAL).
FT DOMAIN 216 231 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 232 259 6 (POTENTIAL).
FT DOMAIN 260 275 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 276 293 7 (POTENTIAL).
FT DOMAIN 294 342 CYTOPLASMIC (POTENTIAL).
FT DISULFID 102 180 BY SIMILARITY.
FT CARBOHYD 16 18 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 342 AA; 39226 MW; 6CBFE389C6E5919E CRC64;

Query Match 31.9%; Score 581; DB 1; Length 342;
Best Local Similarity 34.2%; Pred. No. 8, 1e-29;
Matches 121; Conservative 71; Mismatches 130; Indels 32; Gaps 8;

QY 12 YEEENMGTYDSQYELICIKEDVREFAKVFLPVFLTIVIGLAGNSMVAIYAYK 71
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 6 HYEDGFGFNSDSE-----HDFLOFGKVFPCMLVAVVCGVNSLVLSIFYK 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 72 QRTKTDVYIINLAVALDLLFTLPPMAVNAVHGVNLKIMCKITSALTYNFSGMFLA 131
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 62 LQSLDVFVNLPLADLVFVCTLPFWAVAGIHEWIFGVCMCKTLGLTYTINFTSMILT 121
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 132 CISIDRYVAVTKVPS--QSGVGKPCW--IICFCVMAAIIISTPOLVFTYV--NDNARCI 185
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 122 CTYDREIVVAKATKAVNQAKKMTGKVICLLIWTIVSLVSLVQIIYIGNVFNLDKLC- 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 186 PIFPRYLGTSKKALIMLEICIGFVVPFLMGVCYFTIARTLMKPNIKISRPLKVLTV 245
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 181 ----GYHDEEISTVLAOTMTLGFELPLAMIVCYSVIITKLHAGGFOKHSRLKTIIFV 236
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 246 VIVFIVQLPVNIYKFCALDIILYSLTSCMSKRMALIOVTSIALFHSCNLPILYVF 305
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 237 MAVFLLTQTPENLVKLRSTHMEYAMTSFHYT-----IIVTEALVLRACLPVLYAF 290
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 306 MGASEKNYVMVAKKYG-----SWRROROSEEPFDSKPTSTFSI 350
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 291 VSLKFRKFKMLVNDIGCLPYLGVSHPKSSSEDSK--TFSASHNVEATISMFL 342
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
CCR6_MACMU STANDARD; PRT; 343 AA.
AC 09XTA5;
DB 16-OCT-2001 (Rel. 40, Created)
   16-OCT-2001 (Rel. 40, Last sequence update)
   15-JUN-2002 (Rel. 41, Last annotation update)
   C-X-C chemokine receptor type 6 (CXCR-6) (CXCR-6) (G protein-coupled
   receptor bonzo) (G protein-coupled receptor STRL33).
DB CXCR6 OR BONZO OR STRL33.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21354176; Pubmed=11461684;
RX Margulies B.J., Hauer D.A., Clements J.E.;
RT "Identification and comparison of eleven rhesus macaque chemokine
   receptors."
RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
CC -1- FUNCTION: RECEPTOR FOR THE C-X-C-CHEMOKINE CXCL16. USED AS A
CC CORRECTOR BY SIVS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC EMBL: AF124380; AAD31419.1; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1.1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECPT_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT TRANSMEM 1 33
FT DOMAIN 34 60
FT TRANSMEM 61 69
FT TRANSMEM 70 90
FT DOMAIN 91 104
FT TRANSMEM 105 126
FT DOMAIN 127 144
FT TRANSMEM 145 165
FT TRANSMEM 166 188
FT TRANSMEM 189 216
FT TRANSMEM 217 232
FT TRANSMEM 233 260
FT TRANSMEM 261 276
FT TRANSMEM 277 294
FT DOMAIN 295 343
FT CARBOHYD 17 17
FT DISULFID 103 181
SQ SEQUENCE 343 AA; 39423 MW; 48DB2544949EB83F CRC64;

Query Match 31.4%; Score 571; DB 1; Length 343;
Best Local Similarity 33.4%; Pred. No. 3, 3e-28;
Matches 119; Conservative 73; Mismatches 132; Indels 32; Gaps 8;

QY 10 DYEEENMGTYDSQYELICIKEDVREFAKVFLPVFLTIVIGLAGNSMVAIYAYK 69
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 5 DYEDGFGFNSDSE-----HDFLOFRKVFPCMLVAVVCGVNSLVLSIFY 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 70 KQRTKTDVYIINLAVALDLLFTLPPMAVNAVHGVNLKIMCKITSALTYNFSGMFL 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 61 HKLQSLDVFVNLPLADLVFVCTLPFWAVAGIHEWIFGVCMCKTLGLTYTINFTSMILT 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 130 LACISIDRYVAVTKVPS--QSGVGKPCW--IICFCVMAAIIISTPOLVFTYV--NDNAR 183
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 121 LFCITVDRFIVVAKATKAVNQAKKMTGKVICLLIWTIVSLVSLVQIIYIGNVFNLDKLI 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 184 CIPFPRYLGTSKKALIMLEICIGFVVPFLMGVCYFTIARTLMKPNIKISRPLKVL 243
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 181 C-----GYHDEEISTVLAOTMTLGFELPLAMIVCYSVIITKLHAGGFOKHSRLKTIIF 235
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 244 TVYIVFIVQLPVNIYKFCALDIILYSLTSCMSKRMALIOVTSIALFHSCNLPILY 303
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 236 LVNAVFLLTQTPENLVKLRSTHMEYAMTSFHYT-----IIVTEALVLRACLPVLY 289
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 304 VFMGASEKNYVMVAKKYG-----SWRROROSEEPFDSKPTSTFSI 350
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 290 AFVSLKFRKFKMLVNDIGCLPYLGVSHPKSSSEDSK--TFSASHNVEATISMFL 343
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
CCR6_MACNE STANDARD; PRT; 342 AA.
AC 019024;
DB 15-JUL-1998 (Rel. 36, Created)
   15-JUL-1998 (Rel. 36, Last sequence update)
   15-JUN-2002 (Rel. 41, Last annotation update)
   C-X-C chemokine receptor type 6 (CXCR-6) (CXCR-6) (G protein-coupled
   receptor bonzo).
DB CXCR6 OR BONZO.
OS Macaca nemestrina (pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.

```

| | | |
|----|--|---|
| DR | EMBL; AF007858; AAB64224.1; | - |
| DR | InterPro; IPR000276; GPCR_Rhodopsn. | |
| DR | Pfam; PF00001; 7tm_1; 1. | |
| DR | PRINTS; PR00237; GPCRRHODOPSN. | |
| DR | PROSITE; PS00237; G_PROTEIN_RECIP_FL_1; 1. | |
| DR | PROSITE; PS0262; G_PROTEIN_RECIP_FL_2; 1. | |
| KW | G-protein coupled receptor; Transmembrane; Glycoprotein. | |
| FT | DOMAIN | 1 |
| FT | TRANSMEM | 33 |
| FT | TRANSMEM | 59 |
| FT | TRANSMEM | 69 |
| FT | TRANSMEM | 89 |
| FT | DOMAIN | 90 |
| FT | TRANSMEM | 104 |
| FT | TRANSMEM | 125 |
| FT | DOMAIN | 126 |
| FT | TRANSMEM | 143 |
| FT | TRANSMEM | 144 |
| FT | TRANSMEM | 164 |
| FT | DOMAIN | 165 |
| FT | TRANSMEM | 187 |
| FT | TRANSMEM | 188 |
| FT | DOMAIN | 215 |
| FT | TRANSMEM | 216 |
| FT | TRANSMEM | 232 |
| FT | TRANSMEM | 259 |
| FT | DOMAIN | 260 |
| FT | TRANSMEM | 275 |
| FT | TRANSMEM | 293 |
| FT | TRANSMEM | 294 |
| FT | DISULFD | 342 |
| FT | CARBOHYD | 102 |
| FT | CARBOHYD | 16 |
| FT | CARBOHYD | 16 |
| QO | SEQUENCE | 342 AA; 39297 MW; 35F9FE8CG62D2DF5 CRC64; N-LINKED (GLCNAC...) (POTENTIAL). BY SIMILARITY. |

| | | | | |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match | 31.3%; | Score 569; | DB 1; | length 342; |
| Best Local Similarity | 33.6%; | Pred. No. 4.3e-28; | | |
| Matches 119; | Conservative 72; | Mismatches 131; | Indels 32; | Gaps 8 |

```

0Y      12  YBENENMCTGYVSOYELTICKEDVREKAFKELPVLITVEVGLAGNSMVAIYAYAKK  71
      6  YHEDYGLNFSNDSO-----HÖDFÖRKVELFCMTLVFVCGVGLNSLVIVISIFPK  61
0Y      72  ÖRKTQVYUILLNAVDELLETFPEPMANAVHGVLKIMCKITSALTLYNFGSMÖLA  131
      62  LÖSTIDVELVNLPLADLVAFVCTLPPWAVAGIHEITGÖVWCKILLGVITINFTSMILLT  122
Db      132  C1SIDRYVAVTKVPS--OSGVKPECV--IICFCVMAAILLSIPÖLVFTV--NDMARCI  185
      122  CLIVDBFIVVAVKATYANQÖKRMKWGVICOLLIVISLVSLPÖITGVNVPNDKLIC-  186
0Y      186  PIFPRYLGTSMKALIQMIEICIGVVPRLMGVCYPTANTLKMKNIKISPELVLLTV  245
Db      181  ----GYHDEISTVVLATQMTLGEFLPLAMIVCYSLITILLHAGFGKHSRLIPELV  236
0Y      246  VIVFITYQLPYNIVAFRCRADIITSLTSCMSKRMIDIAQVYESIALFHSLNLIJVF  307
Db      237  MAVEFLLTQPPNVLKRLIRSTHWEYAMTSFHYT-----LIVEEALATYLRACLNPVLYAF  290
0Y      306  MGAFSFKNVYAKKAYG-----SMRÖROSVEEPPDSGCTEPTSTESI  350
Db      291  VSLKFRKNMKVLKVDICCLPIVLGYSHÖKXSEDSK--TTSASHVNEATSMFÖL  342

```

| RESULT 12 | CCRG_HUMAN | STANDARD: | PRT: | 342 AA. |
|-----------|------------|---|------|---------|
| ID | CCRG_HUMAN | 000574; C000575; | | |
| AC | | 15-JUL-1998 (Rel. 36, Created) | | |
| DT | | 15-JUL-1998 (Rel. 36, Last sequence update) | | |
| DT | | 15-JUN-2002 (Rel. 41, Last annotation update) | | |
| DE | | C-X-C chemokine receptor type 6 (CXCR-6) (CXCR-6) (G protein-coupled receptor bonzo) (G protein-coupled receptor STRL33). | | |
| GN | | CXCR6 OR BONZO OR STRL33 OR TYMSR. | | |
| OS | | Homo sapiens (Human). | | |
| OC | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | |
| OX | | NCBI_TaxID:9606; | | |
| RP | | [1] | | |
| RP | | SEQUENCE FROM N.A. | | |
| RX | | MEDLINE=97373958; PubMed=9230441; | | |
| RA | | Deng H.K., Unutuma D., Kewalramani V.N., Littman D.R.; | | |
| RT | | "Expression cloning of new receptors used by simian and human immunodeficiency viruses."; | | |
| RT | | Nature 388:296-300(1997). | | |
| RL | | [2] | | |
| RL | | SEQUENCE FROM N.A. | | |
| RP | | MEDLINE=97311099; PubMed=9166430; | | |
| RX | | Liao F., Alkhalid G., Peden K.W.C., Sharma G., Berger E.A., | | |
| RA | | Farber J.M.; | | |
| RT | | "STRL3, A novel chemokine receptor-like protein, functions as a fusion cofactor for both macrophage-tropic and T cell line-tropic HIV-1."; | | |
| RT | | J. Exp. Med. 185:2015-2023(1997). | | |
| RN | | [3] | | |
| RP | | SEQUENCE FROM N.A. | | |
| RC | | TISSUE=Blood; | | |
| RX | | MEDLINE=97431687; PubMed=9285716; | | |
| RA | | Loetscher M., Amara A., Oberlin E., Brass N., Legler D.F., | | |
| RA | | Loetscher P., D'Amuzio M., Meese E.V., Rouselet D., Virelizier J.L., | | |
| RA | | Baloghlini M., Aranzano-Seisdedos F., Moser B.; | | |
| RT | | "TYMSR, a putative chemokine receptor selectively expressed in activated T cells, exhibits HIV-1 coreceptor function."; | | |
| RT | | Curr. Biol. 7:652-660(1997). | | |
| CC | | -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE CXCL16. USED AS A CORECEPTOR BY SIVS AND BY STRAINS OF HIV-2 AND M-TROPIC HIV-1. | | |
| CC | | -1- SUBCELLULAR LOCATION: Integral membrane protein. | | |
| CC | | -1- TISSUE SPECIFICITY: EXPRESSED IN LYMPHOID TISSUES AND ACTIVATED T CELLS. | | |
| CC | | -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. | | |
| CC | | ----- | | |
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| CC | | ----- | | |
| DR | | EMBL: AF007545; AAB64221.1; - | | |
| DR | | EMBL: U73529; AAB61456.1; - | | |
| DR | | EMBL: U73531; AAB61457.1; - | | |
| DR | | EMBL: Y13248; CAA73698.1; - | | |
| DR | | MIM: 605163; - | | |
| DR | | InterPro: IPR000276; GPCR_Rhodpsn. | | |
| DR | | Pfam: PF00001; 7tm_1; 1. | | |
| DR | | PRINTS: PR00237; GPCRHHODPSN. | | |
| DR | | PROSITE: PS00237; G-PROTEIN_RECCEP_FL1; 1. | | |
| DR | | PROSITE: PS50262; G-PROTEIN_RECCEP_FL2; 1. | | |
| RW | | G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism. | | |
| FT | | DOMAIN 1 32 | | |
| FT | | TRANSMEM 33 59 | | |
| FT | | DOMAIN 60 68 | | |
| FT | | TRANSMEM 69 89 | | |
| FT | | DOMAIN 90 103 | | |
| FT | | TRANSMEM 104 125 | | |
| FT | | DOMAIN 126 143 | | |
| FT | | CYTOPLASMIC (POTENTIAL). | | |
| FT | | CYTOPLASMIC (POTENTIAL). | | |

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FT TRANSMEM 144 164 4 (POTENTIAL).
FT DOMAIN 165 187 5 (POTENTIAL).
FT TRANSMEM 188 215 5 (POTENTIAL).
FT DOMAIN 216 231 6 (POTENTIAL).
FT TRANSMEM 232 259 6 (POTENTIAL).
FT DOMAIN 260 275 7 (POTENTIAL).
FT TRANSMEM 276 293 7 (POTENTIAL).
FT DOMAIN 294 342 7 (POTENTIAL).
FT DISULFID 102 180 7 (POTENTIAL).
FT CARBOHD 16 16 7 (POTENTIAL).
FT VARIANT 25 25 7 (POTENTIAL).
SQ SEQUENCE 342 AA: 39280 MM: /FTID=VAR.003506.
Query Match 30.8%; Score 560; DB 1; Length 342;
Best Local Similarity 33.1%; Pred. No. 1.5e-27;
Matches 117; Conservative 75; Mismatches 130; Indels 32; Gaps 8;
QY 12 YEEENMGNTYDYSOYELICIKEDYREFAKVFPLVPLTIVFVIGLAGSNVVAIYAYKK 71
D 6 YHEDYGFSEFNSQOE---HQDFLOFSKVFPLPCMYLVFVCGLVGNSLVLTISIEYHK 61
QY 72 QRTKDVYILNVAVDLLFLTPWANNVAVGVLKCKITSAKLTLMFVSGMFLA 131
D 62 IQLSLDVFLVNLPLADLVFVCTLPWAVAGLHEWVGWGVCKSLGITYTINFTSMILT 121
QY 133 CISIDRYAVATKVPSS--QSGVGKPCM--IICFCVMAAILSLIPOLVFYTV--NDNARCI 185
D 122 CITVDRFIVVATKAYNOQAKRMVKVSTLLIIVISLVSIPQIITIGNVFNDELKLC- 180
QY 186 PIFPRYLGTSMKALIQMLEICIGFVVPPLMGVCYFIFARLKMKNIKISRPKLVLTV 245
D 181 ----GYHDEAISTVVLATQMTLGFPLPLTLMVCYSVITIKTLHAGGQKRSKLIIFLV 236
QY 246 VIVFVLTQPLVIVFCAIDIIYSLITSCNKRMDIAIOVTEIALFHSCNPIIYVF 305
D 237 MAVFLLTQPLVIVFCAIDIIYSLITSCNKRMDIAIOVTEIALFHSCNPIIYVF 305
QY 306 MGASEKNYMKVAKRYG-----SWRROSVSEEPFSEGTPEPTSFESI 350
D 291 VSLKRKNRWKIVKIDICGLPIYGVSHQKSSBDNSK--TFESAINVENTSMFOL 342
DB 291 VSLKRKNRWKIVKIDICGLPIYGVSHQKSSBDNSK--TFESAINVENTSMFOL 342
RESULT 13
CRR4_HUMAN STANDARD: PRT: 360 AA.
ID CRR4_HUMAN STANDARD: PRT: 360 AA.
AC P51679; G9ULY6; G9ULY7;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 4 (C-C-CCR-4) (CCR-4) (CCR4)
DE (K5-5).
GN CCR4 OR CCKBR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=95370289; PubMed=7642634;
RA Power C.A., Meyer A., Nemeth K.B., Hoogwerf A.J.,
RA Proudfoot A.E.I., Wells T.N.C.;
RT "Molecular cloning and functional expression of a novel CC chemokine
RT receptor cDNA from a human basophilic cell line."
RL J. Biol. Chem. 270:19495-19500(1995).
RN [2]
RP SEQUENCE FROM N.A. AND VARIANTS VAL-130 AND SER-178.
RX MEDLINE=21040311; PubMed=11196669;
RA Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H.,
RA Hirai K., Tokunaga K.;
RT "New variations of human CC-chemokine receptors CCR3 and CCR4."
RL Genes Immun. 1:97-104(1999).

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RN [3]
RP FUNCTION.
RX MEDLINE=97313486; PubMed=9169480;
RA Imai T., Baba M., Nishimura M., Kakizaki M., Takagi S., Yoshie O.;
RT "The T cell-directed CC chemokine TARC is a highly specific
RT biological ligand for CC chemokine receptor 4."
RL J. Biol. Chem. 272:15036-15042(1997).
RN [4]
RP FUNCTION.
RX MEDLINE=98104168; PubMed=9430724;
RA Imai T., Chantry D., Raport C.J., Wood C.L., Nishimura M., Godliska R.,
RA Yoshie O., Gray P.W.;
RT "Macrophage-derived chemokine is a functional ligand for the CC
RT chemokine receptor 4."
RL J. Biol. Chem. 273:1764-1768(1998).
RN [5]
RP FUNCTION.
RX MEDLINE=99394604; PubMed=10466728;
RA Campbell J.J., Haraldsen G., Pan J., Rotman J., Qin S., Ponath P.,
RA Andrew D.P., Wainke R., Ruffing N., Kassam N., Wu L., Butcher E.C.;
RT "The chemokine receptor CCR4 in vascular recognition by cutaneous but
RT not intestinal memory T cells."
RL Nature 400:776-780(1999).
RN [6]
RP FUNCTION. TISSUE SPECIFICITY, AND PHOSPHORYLATION.
RX MEDLINE=20219238; PubMed=10754297;
RA Ingjerdengen M., Damaj B., Maghazachi A.A.;
RT "Human NK cells express CC chemokine receptors 4 and 8 and respond to
RT thymus and activation-regulated chemokine, macrophage-derived
RT chemokine, and I-309."
RL J. Immunol. 164:4048-4054(2000).
RN [7]
RP FUNCTION: HIGH AFFINITY RECEPTOR FOR THE C-C TYPE CHEMOKINES
TARC/SCYA17 AND MDC/SCYA22. THE ACTIVITY OF THIS RECEPTOR IS
MEDIATED BY G(I) PROTEINS WHICH ACTIVATE A PHOSPHATIDYLINOSITO-
CALCIUM SECOND MESSENGER SYSTEM. CAN FUNCTION AS A CHEMOTACTANT
HOMING RECEPTOR ON CIRCULATING MEMORY LYMPHOCYTES AND AS A
CORECEPTOR FOR SOME PRIMARY HIV-2 ISOLATES. IN THE CNS, COULD
MEDIATE HIPPOCAMPAL-NEURON SURVIVAL.
RN [8]
RP SUBCELLULAR LOCATION: Integral membrane protein.
CC TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE THYMUS, IN
PERIPHERAL BLOOD LEUKOCYTES, INCLUDING T CELLS, MOSTLY CD4+ CELLS,
AND BASOPHILS, AND IN PLATELETS; AT LOWER LEVELS, IN THE SPLEEN
AND IN MONOCYTES. DETECTED ALSO IN MACROPHAGES, IL-2-ACTIVATED
NATURAL KILLER CELLS AND SKIN-HOMING MEMORY T CELLS, MOSTLY THE
ONES EXPRESSING THE CUTANEOUS LYMPHOCYTE ANTIGEN (CLA). EXPRESSED
IN BRAIN MICROVASCULAR AND CORONARY ARTERY ENDOTHELIAL CELLS.
CC P.T.M.: IN NATURAL KILLER CELLS, SCYA22 BINDING INDUCES
PHOSPHORYLATION ON YET UNDEFINED SER/THR RESIDUES, MOST PROBABLY
BY BETA-ADRENERGIC RECEPTOR KINASES 1 AND 2.
CC SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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DR EMBL: X65740; CAA59743.1;
DR EMBL: AB023888; BAA86965.1;
DR EMBL: AB023889; BAA86966.1;
DR EMBL: AB023890; BAA86967.1;
DR EMBL: AB023891; BAA86968.1;
DR EMBL: AB023892; BAA86969.1;
DR GeneW: HGNC:1605; CCR4.
DR MIM: 604836;
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1.1.
DR PRINTS: PR00237; GPCRHOPOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECPT_FL1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECPT_FL2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein;
KW

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FT TRANSMEM 85 105 2 (POTENTIAL).
FT DOMAIN 106 120 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 121 142 3 (POTENTIAL).
FT DOMAIN 143 163 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 164 183 4 (POTENTIAL).
FT DOMAIN 184 208 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 209 231 5 (POTENTIAL).
FT DOMAIN 232 251 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 252 273 6 (POTENTIAL).
FT DOMAIN 274 294 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 295 315 7 (POTENTIAL).
FT DOMAIN 316 360 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 119 196 BY SIMILARITY.
SQ SEQUENCE 360 AA; 40759 MW; 564F04ABBC0A197 CRC64;

Query Match 29.4%; Score 534.5; DB 1; Length 360;
Best Local Similarity 33.2%; Pred. No. 5.5e-26;
Matches 120; Conservative 75; Mismatches 141; Indels 25; Gaps 8;

QY 3 LEONOSTDYEEENEMNGTYDSQYELI-----CIKEDVREFAKVFLPFLTIYVIGLA 57
DB 6 MESDFEDFMKGEDLSNYSYSTLPFLDAPCEPSL-EINKYFVITVALVFLSL 64
QY 58 GNSVVAIYAYKKORTDYIILNLAVALDLLFTLPMAVNAHGVKIGKICKITSA 117
DB 65 GNSLWLVILSVRSVSTVDYLLNLAVALDLLFTLPMAVNAHGVKIGKICKITSA 124
QY 118 LYTINFSVSMQFLACISIDRYAVV---TKVPSOGVGKPCWITFCVMAAILISIPOLY 174
DB 125 LKEVNFYSGILLACISIDRYAVV---TKVPSOGVGKPCWITFCVMAAILISIPOLY 182
QY 175 F---YVNDNARCIPFRYGLG---TSMKALIQMLEICIGVFPFLMGVCFITARTL 227
DB 183 FRRTYVSSNVSPACY---EDMGNNNTAMWMLRLPQSEGFIVPLIMLFCYGTLTTL 238
QY 228 MKMPNIRKISRPKLVIYVIVTQLPYINVKFCRAIDIIYLSITSCNMSKRDIAIOV 287
DB 239 FKAHMGQKRRAMRVFAVAVLFLCMLPYNLVLAIDLMTQVIOECERNHIDRALDA 298
QY 288 TESTALFHSCLNPLIYVFMGASFKNVYKAVKYGSMRQ---RQSYEEFPDESGTPEP 344
DB 299 TELIGILHSCNPLIYAFIGQKFRHGLKILAIHGLISKDSLPRDSRPVSGSSGHTST 358
QY 345 T 345
DB 359 T 359

RESULT 15
IL8B_PANTR 1L8B_PANTR STANDARD; PRT; 353 AA.
AC Q28807;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE High affinity Interleukin-8 receptor B (IL-8R B) (CXCR-2) (Fragment).
GN IL8RB OR CXCR2.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
OC NCBI_TaxID=9598;
RX MEDLINE=96175151; PubMed=9110929;
RA Alvarez V., Coto E., Sellen F., Gonzalez S., Gonzalez-Roces S.,
RA Lopez-Larrea C.;
RT "Characterization of interleukin-8 receptors in non-human primates.";
RL Immunogenetics 43:261-267(1996).
CC -I- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND

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CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
CC THIS SWISS-PROT ENTRY IS COPYRIGHT. IT IS PRODUCED THROUGH A COLLABORATION
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CC
CC EMBL: X91113; CA62563.1; -.
CC HSSP: P34996; 1DDO.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR InterPro: IPR000832; GPCR_secretin.
DR Pfam: PF00001; 7tm_1.1.
DR PROSITE: PS00237; G_PROTEIN_RECPEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECPEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Chemotaxis.
FT NON_TER 1 1
FT TRANSMEM 46 72 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 73 81 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 82 102 2 (POTENTIAL).
FT DOMAIN 103 117 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 118 139 3 (POTENTIAL).
FT DOMAIN 140 160 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 161 180 4 (POTENTIAL).
FT DOMAIN 181 205 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 206 228 5 (POTENTIAL).
FT TRANSMEM 229 248 6 (POTENTIAL).
FT TRANSMEM 249 270 6 (POTENTIAL).
FT DOMAIN 271 291 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 292 312 7 (POTENTIAL).
FT DOMAIN 313 >353 CYTOPLASMIC (POTENTIAL).
FT DISULFID 116 193 BY SIMILARITY.
FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 353 353
SQ SEQUENCE 353 AA; 39998 MW; E745ACD9EC10C1E2 CRC64;

Query Match 29.1%; Score 529.5; DB 1; Length 353;
Best Local Similarity 33.6%; Pred. No. 1.1e-25;
Matches 118; Conservative 74; Mismatches 132; Indels 27; Gaps 8;

QY 3 LEONOSTDYEEENEMNGTYDSQYELI-----CIKEDVREFAKVFLPFLTIYVIGLA 57
DB 3 MESDFEDFMKGEDLSNYSYSTLPFLDAPCEPSL-EINKYFVITVALVFLSL 61
QY 58 GNSVVAIYAYKKORTDYIILNLAVALDLLFTLPMAVNAHGVKIGKICKITSA 117
DB 62 GNSLWLVILSVRSVSTVDYLLNLAVALDLLFTLPMAVNAHGVKIGKICKITSA 121
QY 118 LYTINFSVSMQFLACISIDRYAVV---TKVPSOGVGKPCWITFCVMAAILISIPOLY 174
DB 122 LKEVNFYSGILLACISIDRYAVV---TKVPSOGVGKPCWITFCVMAAILISIPOLY 179
QY 175 F---YVNDNARCIPFRYGLG---TSMKALIQMLEICIGVFPFLMGVCFITARTL 227
DB 180 FRRTYVSSNVSPACY---EDMGNNNTAMWMLRLPQSEGFIVPLIMLFCYGTLTTL 235
QY 228 MKMPNIRKISRPKLVIYVIVTQLPYINVKFCRAIDIIYLSITSCNMSKRDIAIOV 287
DB 236 FKAHMGQKRRAMRVFAVAVLFLCMLPYNLVLAIDLMTQVIOECERNHIDRALDA 295
QY 288 TESTALFHSCLNPLIYVFMGASFKNVYKAVKYGSMRQ---RQSYEEFPDESGTPEP 338
DB 296 TELIGILHSCNPLIYAFIGQKFRHGLKILAIHGLISKDSLPRDSRPVSGSSGHTST 341

Search completed: March 14, 2003, 16:11:45

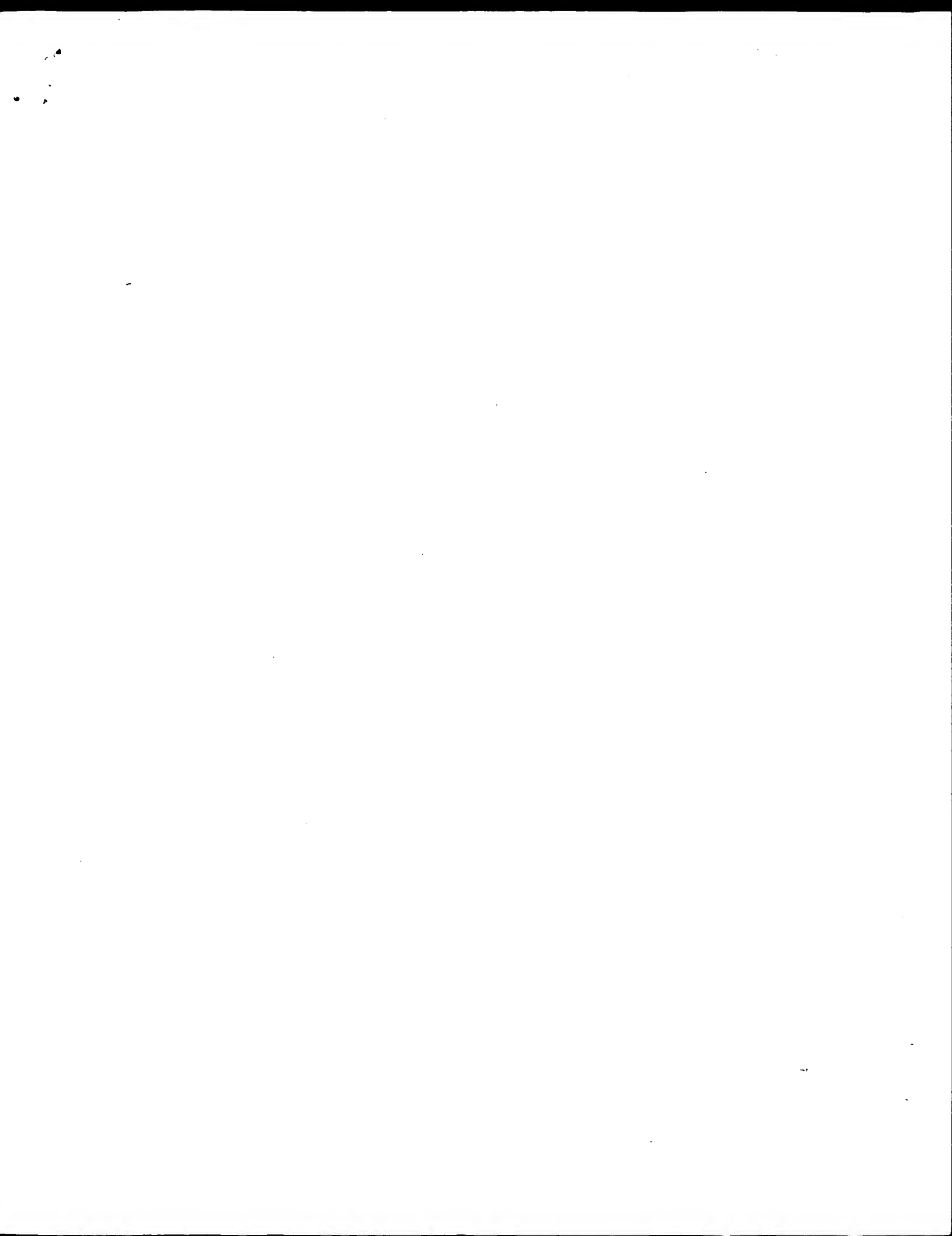
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Mon Mar 17 12:24:55 2003

us-09-686-020a-2.rsp

Page 13

Job time : 13 secs



GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 16:10:47 ; Search time 19 Seconds
(without alignments)
1770.897 Million cell updates/sec

Title: US-09-686-020A-2

Perfect score: 1819

Sequence: 1 MALEQNSTDYEEENMNG.....VEEPFDSGPTPTSTFST 350

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|----------------------|
| 1 | 1620 | 89.1 | 350 | 2 JN0621 | G protein-coupled |
| 2 | 659 | 36.7 | 378 | 2 B55735 | lymphocyte-specific |
| 3 | 650 | 35.7 | 378 | 2 A55735 | G protein-coupled |
| 4 | 643 | 35.3 | 378 | 2 A45680 | G protein-coupled |
| 5 | 583 | 32.1 | 369 | 2 JC5068 | chemokine (C-C) re |
| 6 | 537.5 | 29.5 | 360 | 2 A57160 | interleukin-8 rece |
| 7 | 534.5 | 29.4 | 360 | 2 A53611 | interleukin-8 rece |
| 8 | 524 | 28.8 | 354 | 2 J58186 | probable G protein-c |
| 9 | 522.5 | 28.7 | 352 | 2 JC4304 | orphan G protein-c |
| 10 | 522.5 | 28.7 | 360 | 2 JC4587 | chemokine (C-C) re |
| 11 | 518.5 | 28.5 | 354 | 2 B55735 | G protein-coupled |
| 12 | 511 | 28.1 | 358 | 2 A53752 | interleukin-8 rece |
| 13 | 501.5 | 27.6 | 355 | 2 JQ1231 | interleukin-8 rece |
| 14 | 500.5 | 27.5 | 352 | 2 A45747 | neuropeptide Y/pep |
| 15 | 499.5 | 27.5 | 353 | 2 S28787 | neuropeptide Y/pep |
| 16 | 493.5 | 27.1 | 352 | 2 G00048 | fusin (LESTRA) - C |
| 17 | 492 | 27.0 | 360 | 2 JC2443 | chemokine (C-C) re |
| 18 | 489.5 | 26.9 | 350 | 2 A39445 | interleukin-8 rece |
| 19 | 486 | 26.7 | 355 | 2 JC5067 | G protein-coupled |
| 20 | 485 | 26.6 | 355 | 2 A49339 | macrophage inflamm |
| 21 | 484.5 | 26.6 | 352 | 2 A43113 | chemokine (C-C) re |
| 22 | 483.5 | 26.6 | 359 | 2 A48921 | interleukin-8 rece |
| 23 | 482 | 26.5 | 374 | 2 I38450 | chemokine (C-C) re |
| 24 | 479.5 | 26.4 | 359 | 2 I49341 | MIP-1 alpha recept |
| 25 | 476.5 | 26.2 | 367 | 2 JE0349 | interferon-inducib |
| 26 | 474 | 26.1 | 355 | 2 A45177 | chemokine (C-C) re |
| 27 | 471 | 25.9 | 356 | 2 S42096 | interleukin-8 rece |
| 28 | 470 | 25.8 | 383 | 2 S55594 | G protein-coupled |
| 29 | 461.5 | 25.4 | 355 | 2 G02436 | chemokine (C-C) re |

| | | | | | |
|----|-------|------|-----|----------|--------------------|
| 30 | 455.5 | 25.0 | 359 | 2 S44425 | angiotensin II rec |
| 31 | 452.5 | 24.9 | 359 | 2 JC1104 | angiotensin II rec |
| 32 | 452.5 | 24.9 | 359 | 2 JC2134 | angiotensin II rec |
| 33 | 450 | 24.7 | 359 | 2 S15403 | angiotensin II rec |
| 34 | 450 | 24.7 | 374 | 2 S32785 | G protein-coupled |
| 35 | 446.5 | 24.5 | 359 | 2 A48857 | angiotensin II rec |
| 36 | 445.5 | 24.5 | 356 | 2 I49340 | MIP-1 alpha recept |
| 37 | 442.5 | 24.3 | 372 | 2 S26657 | G protein-coupled |
| 38 | 442.5 | 24.3 | 374 | 2 S42628 | G protein-coupled |
| 39 | 441 | 24.2 | 362 | 2 JN0694 | angiotensin II rec |
| 40 | 439 | 24.1 | 359 | 2 A42656 | angiotensin II rec |
| 41 | 438.5 | 24.1 | 359 | 2 JH0621 | angiotensin II rec |
| 42 | 438.5 | 24.1 | 362 | 2 A39714 | G protein-coupled |
| 43 | 437.5 | 24.1 | 327 | 2 S56162 | MDCR15 protein - h |
| 44 | 434 | 23.9 | 359 | 2 J01516 | angiotensin II rec |
| 45 | 428.5 | 23.6 | 359 | 2 I39418 | angiotensin II rec |

ALIGNMENTS

RESULT 1

JN0621
G protein-coupled receptor type B - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 19-May-2000
C:Accession: JN0621
R:Matsuroka, I.; Mori, T.; Aoki, J.; Sato, T.; Kurihara, K. ;
Biochem. Biophys. Res. Commun. 194, 504-511, 1993
A:Title: Identification of novel members of G-protein coupled receptor superfamily ex
A:Reference number: JN0621; MUID:93326166; PMID:8392843
A:Accession: JN0621
A:Molecule type: mRNA
A:Residues: 1-350 <MAT>
A:Cross-references: GB:563848; NID:9399710; PIDN:AAB2547.1; PID:9399711
A:Experimental source: tongue taste papillae
A:Comment: This protein is involved in modulating taste sensitivity or regeneration o
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein
F:42-66/Domain: transmembrane #status predicted <TM1>
F:80-99/Domain: transmembrane #status predicted <TM2>
F:114-135/Domain: transmembrane #status predicted <TM3>
F:154-175/Domain: transmembrane #status predicted <TM4>
F:200-222/Domain: transmembrane #status predicted <TM5>
F:242-265/Domain: transmembrane #status predicted <TM6>
F:284-306/Domain: transmembrane #status predicted <TM7>
F:6.19/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 89.1%; Score 1620; DB 2; Length 350;

Best Local Similarity 86.0%; Pred. No. 1.3e-131;
Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| QY | 1 | MALEQNSTDYEEENMNGTYSOVELCTIEDREFKAVLPVFTVIFVIGLAGNS | 60 |
| DB | 1 | MAVEYNSTDYEEENMNDTHDYSOEVCIEEVRKFAKVLPAFFTAFTIGLAGNS | 60 |
| QY | 61 | MVAIVAYVYKKRKRTDVTLLNLAVALDLLFTLPMAVAVAGVVLGKIMCKTSALYT | 120 |
| DB | 61 | TVAIVAYVYKKRKRTDVTLLNLAVALDLLFTLPMAVAVAGVVLGKIMCKTSALYT | 120 |
| QY | 121 | LNFVSGMQLACISIDRYAVAVTKVPSSGSGKRCMCIICVMAAALLSPVLQFTVND | 180 |
| DB | 61 | TVAIVAYVYKKRKRTDVTLLNLAVALDLLFTLPMAVAVAGVVLGKIMCKTSALYT | 120 |
| QY | 121 | VNFVSGMQLACISIDRYAVAVTKVPSSGSGKRCMCIICVMAAALLSPVLQFTVND | 180 |
| DB | 121 | VNFVSGMQLACISIDRYAVAVTKVPSSGSGKRCMCIICVMAAALLSPVLQFTVND | 180 |
| QY | 181 | NARCIPFEPYVLTGSMKALOMLETCIGFVPPPLINGVCFTARTLMKPNKISRPLK | 240 |
| DB | 181 | KARCVPLFEPYVLTGSMKALOMLETCIGFVPPPLINGVCFTARTLMKPNKISRPLK | 240 |
| QY | 241 | VLLTVVIVFTVQLPYNIVKFCRAIDITVSLTSCMKSMDIAIOVTSIALFHSCLNP | 300 |
| DB | 241 | VLLTVVIVFTVQLPYNIVKFCRAIDITVSLTSCMKSMDIAIOVTSIALFHSCLNP | 300 |
| QY | 301 | ILYVKGASFKNTVMKAYKGSRRORQSVVEEPFDSGPTPTSTFST 350 | |

Db 301 VLAVFMGTSFKNYIMKAKKXGSMWRORONVEIPEFSEDATEPTSTFSI 350

RESULT 2

Lymphocyte-specific G protein-coupled receptor EB11 - human
 A:Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1
 C:Species: Homo sapiens (man)
 C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000
 C:Accession: B55735; S52443
 R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
 Genomics 23, 643-650, 1994
 A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor
 A:Reference number: A55735; MUID:95154835; PMID:7851893
 A:Accession: B55735
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-378 <SCH>
 A:Cross-references: GB:L31581; NID:g468319; PIDN:AAA74231.1; PID:g468320
 R:Burgstahler, R.; Kempkes, B.; Staube, K.; Lipp, M.
 Submitted to the EMBL Data Library, February 1995
 A:Description: The expression of the chemokine receptor BLR2/EB11 is specifically trans-
 A:Reference number: S52443
 A:Accession: S52443
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 21-378 <BUR>
 A:Cross-references: EMBL:X84702
 C:Genetics:
 A:Gene: GDB:CMKBR7; EBI1; BLR2; CCR7
 A:Cross-references: GDB:342065; OMIM:600242
 A:Map position: 17q12-17q21.2
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor

Query Match 36.2%; Score 659; DB 2; Length 378;

Best Local Similarity 38.7%; Pred. No. 4.8e-49; Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

Qy 1 MALBONSTDYVEENEMNGTYDYSOYELICIKEDVREFAKVPFLVPLTIVFVIGLAGNS 60
 Db 21 VCLQDEVTDDYIGDNT---TVDTLIESCSKRDVNFKAMFLPMYSLICFVGLGNG 77
 Qy 61 MVVAIAYKKKRTKTDVYLINLAVADLLFLTPMAVNAVHGVLGKIMCKITTSALYT 120
 Db 78 LVVLTLYIFKRLKMTDTYLLNLAVADLLFLTPMAVSAKSWVGVHFKLIPAIYK 137
 Qy 121 LNFVSGQFLACISIDRYVAVTKPS---QSGVGRPCWITICCVMAAILLSIPOLVFY 176
 Db 138 MSFPGSNVLLLCISIDRYVAIVQAVSAHRHRAVLLISLSCVGIWILATVLSIPELLYS 197
 Qy 177 TVNNA-----RCIPFPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYTFARTLMKMP 231
 Db 198 DLOSSSEBQARCLITEH---VEAFITQYQAVNIFVLPVLAMSCYIVITRTLLQAR 254
 Qy 232 NIKISRLKVLVIVIVITQLPYNTVKECRAIDIIYSLITSCNMSKRDIAIQVTESI 291
 Db 255 NFEERNKAIVIAVIVVEIYQLPYNGVLAQVYANFNITSSCELSKQINIAVDYVSL 314
 Qy 292 ALPHSCNPLIYVMGSAFKNYVKKVAKKG-----SW-----RRROSVVEEPFD 337
 Db 315 ACVRCNVNPELYAFIVGKFRNDLFKLDGLCSOLOLRWSSCRHIRSSMSVE----- 369
 Qy 338 SEGETEPTSTFS 349
 Db 370 -----AETTTTFS 377

RESULT 3
 A55735
 G protein-coupled receptor EBI1 - mouse
 C:Species: Mus musculus (house mouse)

C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999
 C:Accession: A55735

R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.
 Genomics 23, 643-650, 1994
 A:Title: Cloning of human and mouse EBI1, a lymphoid-specific G-protein-coupled recep
 A:Reference number: A55735; MUID:95154835; PMID:7851893
 A:Accession: A55735
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-378 <SCH>

A:Cross-references: GB:L31580; NID:g468340; PIDN:AAA74232.1; PID:g468341
 A:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor

Query Match 35.7%; Score 650; DB 2; Length 378;

Best Local Similarity 38.3%; Pred. No. 2.8e-48; Matches 140; Conservative 67; Mismatches 125; Indels 34; Gaps 8;

Qy 5 QNSTDYVEENEMNGTYDYSOYELICIKEDVREFAKVPFLVPLTIVFVIGLAGNSMYVA 64
 Db 25 QDEVTDYIGENT---TVDTLIESVCFKRDVNFKAMFLPMYSLICFVGLGNGVIL 81
 Qy 65 IYVYKKKRTKTDVYLINLAVADLLFLTPMAVNAVHGVLGKIMCKITTSALTNFV 124
 Db 82 TYIFKRLKMTDTYLLNLAVADLLFLTPMAVSEAKSWVGVHFKLIPAIYK 141
 Qy 125 SGMOFLACISIDRYVAVTKPSQSG-----VGRPCWITICCVMAAILLSIPOLVFY 177
 Db 142 SGMLLLCISIDRYVAIVQAVSAHRHRAVLLISK---LSCGIMMALFLSIPELLYSG 198
 Qy 178 VNDNA-----RCIPFPRYLGTSMKAL--IQMLEICIGFVVPFLIMGVCYTFARTLMK 230
 Db 199 LQNSGEDTLRC-----SLVSAQVEALTIQYQAVGFLVPLMAMSCYILITRTLLQA 253
 Qy 231 PNKISRPLKVLTVYIVITQLPYNTVKECRAIDIIYSLITSCNMSKRDIAIQVTE 290
 Db 254 RNFERRKAKIVIAVIVVEIYQLPYNGVLAQVYANFNITSSCELSKQINIAVDYVS 313
 Qy 291 IALFHSCLNPLIYVMGSAFKNYVKKVAKKXGSMWROR-----QSVVEEPFDEGPT 343
 Db 314 LASVRCNVNPELYAFIVGKFRSDLFKLDGLCSQERLRHMSCRHIRNMSVSN---AE 371
 Qy 344 PTSTFS 349
 Db 372 TTTTFS 377

RESULT 4

A45680
 G protein-coupled peptide receptor EBI 1 - human

C:Species: Homo sapiens (man)
 C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
 C:Accession: A45680
 R:Birenbach, M.; Jørgensen, K.; Yalamanchili, R.; Lenoir, G.; Kieff, E.
 J. Virol. 67, 2209-2220, 1993

A:Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-couple
 A:Reference number: A45680; MUID:93188173; PMID:8383238
 A:Accession: A45680
 A:Status: preliminary

A:Molecule type: nucleic acid
 A:Residues: 1-378 <BIR>
 A:Cross-references: GB:L08176; NID:g183484; PID:g183485
 A:Experimental source: B-lymphocytes
 A:Note: sequence extracted from NCBI backbone (NCBI:127094, NCBI:127095)
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 35.3%; Score 643; DB 2; Length 378;

Best Local Similarity 39.0%; Pred. No. 1.1e-47; Matches 145; Conservative 62; Mismatches 127; Indels 38; Gaps 8;

Qy 1 MALBONSTDYVEENEMNGTYDYSOYELICIKEDVREFAKVPFLVPLTIVFVIGLAGNS 60
 Db 21 VCLQDEVTDDYIGDNT---TVDTLIESCSKRDVNFKAMFLPMYSLICFVGLGNG 77

Db 21 VCLCODEVTDYIDGNT---TVDYTFESLCSKDVNFKAMELPIMKSIICEVGLGNG 77
 QY 61 MVAATAYAYKORRTDYIILNLAVALDLEFLLPFAVNAVNAHVGKIMCKITSAIYT 120
 Db 78 LVLTLTYIFKRTKMTDYILNLAVALDLEFLLPFAVNAVNAHVGKIMCKITSAIYT 137
 QY 121 LNFVSGMOLACISIDRYVAATKVSQSGVKPCMTI--CFCVMA--ALLSTPOLVFY 176
 Db 138 MSFSGMILLICISIDRYVAATKVSQSGVKPCMTI--CFCVMA--ALLSTPOLVFY 197
 QY 177 TVNDA-----RCPIPRYIGTSMKALICIGFVPELIMGVCFYFARTLMKMP 231
 Db 198 DLQRSSSQAMKCSLITEH---VEAFITIOVAQWIGFVLPLAMSPCYLITLILQAR 254
 QY 232 NIKIRPRLKVLTVYIVTOLPYNIYFCRAIDIIYSLTSCMSKRDIAIOVTESTI 291
 Db 255 NERKKAIVIAVAVVVFVLPNGVLAQTVANFNITSTELSKOLINADVITSL 314
 QY 292 ALPHSCNPLILYFVGASKRNYVMVAKKYG-----SW-----BRQSVPEFPFD 337
 Db 315 ACVRCVNPFLAFYGVFRNDIFKFLDGLGLOEQDLRQMSCKRHRIRSKSYE----- 369
 QY 338 SEGPEPTSTFS 349
 Db 370 ----AETTTFS 377

RESULT 5

JC5068
 G protein-coupled receptor CRK-L3 - human
 C:Species: Homo sapiens (man)
 C>Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
 C:Accession: J03068
 R:Zaballios, A.; Vatrona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
 Biochem. Biophys. Res. Commun. 227, 846-853, 1996
 A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-like
 A:Reference number: JC5067; MUID:97040707; PMID:886020
 A:Accession: J03068
 A:Molecule type: DNA
 A:Residues: 1-369 <ZAB>
 A:Cross-references: EMBL:279784; NID:91668737; PIDN:CAB02144.1; PID:91668738
 C:Comment: This protein belongs to the family of alpha chemokine receptors.
 C:Genetics:
 A:Gene: GDB:CMKBR6; STRL22; GPR29; CCR6; CRK-L3; GPR-CY4
 A:Cross-references: GDB:5370639; OMIM:601835
 A:Map position: 6q27-6q27
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein
 F:42-68/Domain: transmembrane #status predicted <TM1>
 F:79-99/Domain: transmembrane #status predicted <TM2>
 F:115-136/Domain: transmembrane #status predicted <TM3>
 F:160-180/Domain: transmembrane #status predicted <TM4>
 F:212-233/Domain: transmembrane #status predicted <TM5>
 F:250-271/Domain: transmembrane #status predicted <TM6>
 F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match 32.1%; Score 583; DB 2; Length 369;
 Best local similarity 36.1%; Pred. No. 1.6e-42;
 Matches 121; Conservative 68; Mismatches 120; Indels 26; Gaps 7;

QY 8 STDYVEENMGNGTYDYSEYELICIKEDVREPAKFLPVLTVYFVIGLAGNSMVAIYA 67
 Db 18 NTSYYSVDESE-----LLCSIOEVRKPSFLPVLPIYSLVCEVGLGNTLVITTEA 67
 QY 68 YRKORFTDYIILNLAVALDLEFLLPFAVNAVNAHVGKIMCKITSAIYT 126
 Db 68 FYKARSMTDYIILNLAVALDLEFLLPFAVNAVNAHVGKIMCKITSAIYT 127
 QY 127 MQLACISIDRYVAATKVSQSGVKPCMTI--CFCVMA--ALLSTPOLVFY 179
 Db 128 MLLTLCISMDRYIAIVATKVSFRLSRITLPSKILICLVVGLSVLITSSSTFVFNOKYNTQ 187
 QY 180 DNACIPIPRYIGTSMKALICIGFVPELIMGVCFYFARTLMKMPNIKI 235

Db 188 GSDVC---EKRYQVSEPIRPMKLMGLLEFELFPLMFIFCYFYKTLVQAQNSKR 244
 QY 236 SRPLKVLTVYIVTOLPYNIYFCRAIDIIYSLTSCMSKRDIAIOVTESTI 295
 Db 245 HKAIRVIAVAVVVFVLPNGVLAQTVANFNITSTELSKOLINADVITSL 314
 QY 296 SCNPLILYFVGASKRNYVMVAKKYG-----SW-----BRQSVPEFPFD 337
 Db 304 CCLNPVLAFTIGOKFRNIFLTKDLKMCVRRKKS 338

RESULT 6

A57160
 chemokine (C-C) receptor 4 - human
 N:Alternate names: C-C CRK-4
 C:Species: Homo sapiens (man)
 C>Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
 C:Accession: A57160
 R:Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.
 J. Biol. Chem. 270, 19495-19500, 1995
 A:Title: Molecular cloning and functional expression of a novel CC chemokine receptor
 A:Reference number: A57160; MUID:95370289; PMID:7642634
 A:Accession: A57160
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-360 <POM>
 A:Cross-references: GB:X85740; NID:91370103; PIDN:CAA59743.1; PID:9971452
 A:Note: source clone K5-5
 C:Genetics:
 A:Gene: GDB:CMKBR4
 A:Cross-references: GDB:677463
 A:Map position: 3p21-3p21
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane p
 F:40-65/Domain: transmembrane #status predicted <TM1>
 F:76-97/Domain: transmembrane #status predicted <TM2>
 F:112-133/Domain: transmembrane #status predicted <TM3>
 F:151-175/Domain: transmembrane #status predicted <TM4>
 F:208-226/Domain: transmembrane #status predicted <TM5>
 F:243-264/Domain: transmembrane #status predicted <TM6>
 F:291-308/Domain: transmembrane #status predicted <TM7>
 F:29-376.110-187/disulfide bonds: #status predicted
 F:72.350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predi
 F:143/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predi
 F:183.194/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predi

Query Match 29.5%; Score 537.5; DB 2; Length 360;
 Best local similarity 35.8%; Pred. No. 1.2e-38;
 Matches 115; Conservative 63; Mismatches 124; Indels 19; Gaps 6;

QY 10 DYVEENMGNGTYDYSEYELICIKEDVREPAKFLPVLTVYFVIGLAGNSMVAIYA 69
 Db 8 DTLDESIYSNLYVESIPKPKCKGKAFGLFLPPLYSILVFGGLGNSVVAIYLFKY 67
 QY 70 KROKRTDYIILNLAVALDLEFLLPFAVNAVNAHVGKIMCKITSAIYT 129
 Db 68 KRLRSMTDYIILNLAVALDLEFLLPFAVNAVNAHVGKIMCKITSAIYT 127
 QY 130 LACISIDRYVAATKVSQSGVKPCMTI--CFCVMA--ALLSTPOLVFY 179
 Db 128 VMLMSIDRLALVAHVSRLARTLYGV-----ITSLATWSVAVPAASLPGLFSTCYTER 182
 QY 180 DNACIPIPRYIGTSMKALICIGFVPELIMGVCFYFARTLMKMPNIKI 238
 Db 183 NHTYCKTKYS--LNSYTWKVLSSLEINILGLVILPGLMFCSMILRLOHCKNKKAKA 240
 QY 239 LKVLTLVTVYIVTOLPYNIYFCRAIDIIYSLTSCMSKRDIAIOVTESTI 298
 Db 241 VKMIRAVVAVVVFVLPNGVLAQTVANFNITSTELSKOLINADVITSL 314
 QY 299 NPLVYFVGASKRNYVMVAKKYG-----SW-----BRQSVPEFPFD 337

A:Residues: 1-352 <RES>
A:Cross-references: GB:D01639; NID:g189313; PIDN:AAA16594.1; PID:g189314
R:Nomura, H.; Nielsen, B.W.; Matsushima, K.
Int. Immunol. 5, 1239-1249, 1993
A:Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte chem
A:Reference number: 154751; MUID:94092629; PMID:7505609
A:Accession: 169203
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-352 <RES>
A:Cross-references: GB:D10924; NID:g219868; PIDN:BA01722.1; PID:g219869
C:Genetics:
A:Gene: GDB:NPY3R; NPY3
A:Cross-references: GDB:230002; OMIM:162643
A:Map position: 2q21-2q21
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 27.5%; Score 500.5; DB 2; Length 352;
Best Local Similarity 34.6%; Pred. No. 1.8e-35;
Matches 107; Conservative 57; Mismatches 134; Indels 11; Gaps 4;

QY 8 STDYVEENENGTVDYSQYELICIKEDVREFAKVPFLVFLTVFVIGLAGNSMVAIYA 67
DB 8 TSDNYTEE--MGSGDYDSMKPCFRENANFNKIFLPTYSIFLTGIVNGVLVIMG 64
QY 68 YKKQRTDVTYIILNLAVALDLLFTLPFAVNAVHGVGLGKIMCKITSAITYLTFVSGM 127
DB 65 YOKLRSMTDYRLHLVSADLLFVTLPEFAVDNAVHGVGLGKIMCKITSAITYLTVNLSSV 124
QY 128 QFLACISIDRYVAATKVSQSGVGKPC--WICFCVMAAIIISIPOLVEFTV--NDNA 182
DB 125 LIAFISIDRYLAIVHATNSORPKRLAEKVVYGVWIPALLTIPDFIFANVSEADRY 184
QY 183 RCIPFPYLGTSKALIQMLEICIGFVVPFLMGVCYFITARLMMKPNKISRPLKVL 242
DB 185 ICDREFPNDLWV--VVFQFQHIWGLIPGILSCYCIISKLSHSGHQRKALKTT 241
QY 243 LTVVFTVTOLPYNIYVFCRAIDYISLITSCNMSKRMIDIAIOVTSIALFHSCLPIL 302
DB 242 VILIAFACMLPYIIGISIDSFILEITIKOGCEFEFTVHKWISITETALAFHCCLPIL 301
QY 303 YFMGASFK 311
DB 302 YAFUGAKFK 310

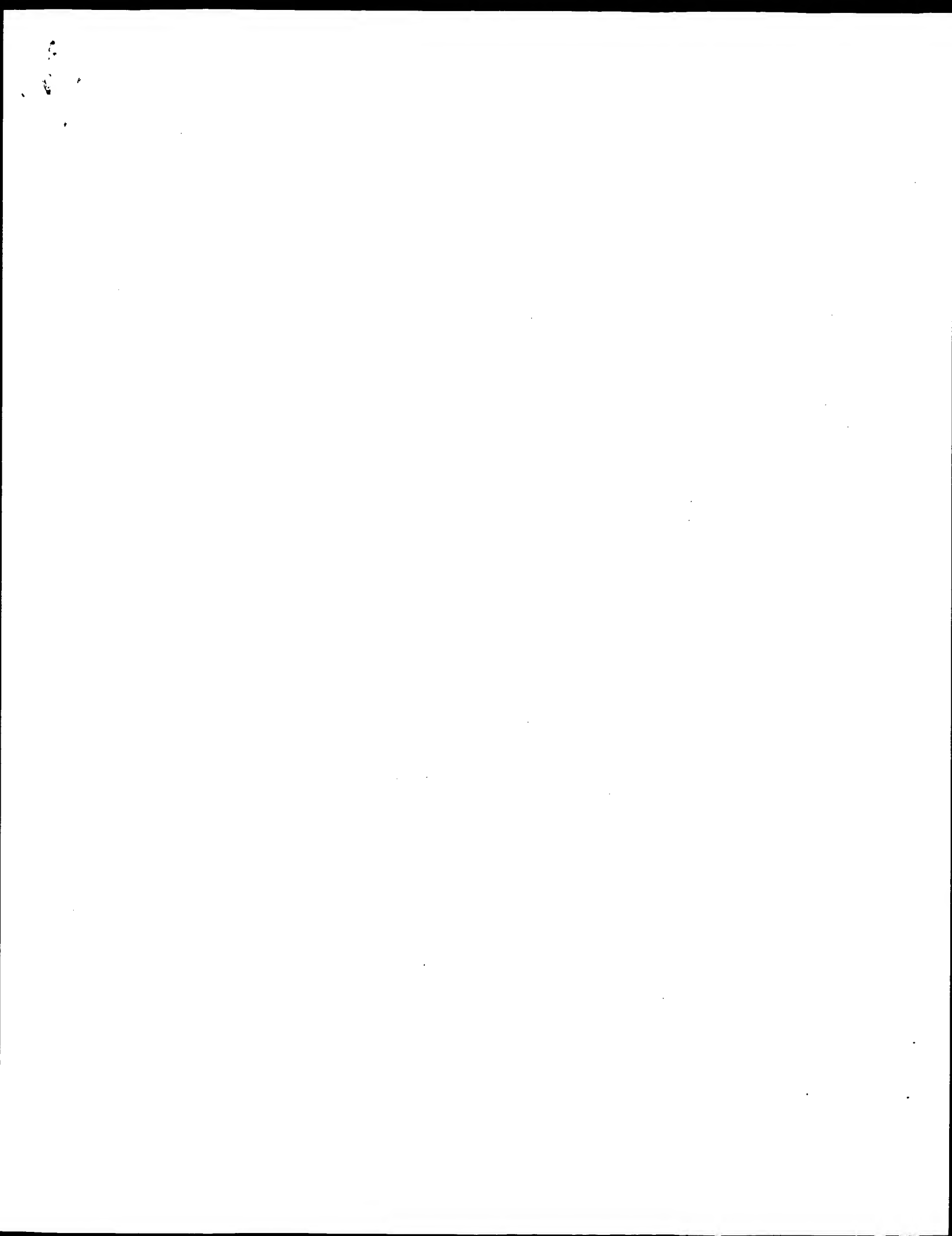
RESULT 15
S28787
neuropeptide Y/peptide YY receptor Y3 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 17-Apr-1993 #sequence-revision 17-Apr-1993 #text-change 26-Aug-1999
C:Accession: S28787
R:Rimland, J.; Xin, W.; Sweetnam, P.; Saljoh, K.; Nestler, E.J.; Duman, R.S.
Mol. Pharmacol. 40, 869-875, 1991
A:Title: Sequence and expression of a neuropeptide Y receptor cDNA.
A:Reference number: S28787; MUID:92100053; PMID:1661837
A:Accession: S28787
A:Molecule type: mRNA
A:Residues: 1-353 <RIM>
A:Cross-references: EMBL:M86739
C:Superfamily: vertebrate rhodopsin
C:Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match 27.5%; Score 499.5; DB 2; Length 353;
Best Local Similarity 34.5%; Pred. No. 2.2e-35;
Matches 106; Conservative 60; Mismatches 126; Indels 15; Gaps 5;

QY 13 YEENENGTVDYSQYELICIKEDVREFAKVPFLVFLTVFVIGLAGNSMVAIYAAYYKQ 72
DB 12 YTEDDL-GSGDYDSMKPCFRENANFNKIFLPTYSIFLTGIVNGVLVIMGYOKKL 70
QY 73 RRTDVTYIILNLAVALDLLFTLPFAVNAVHGVGLGKIMCKITSAITYLTVNLSSVGLAC 132

DB 71 RSMTEKYRLHLVSADLLFVTLPEFAVDNAVHGVGLGKIMCKITSAITYLTVNLSSVGLAC 130
QY 133 ISIDRYVAATKVPVSQSGVGKPC-----WICFCVMAAIIISIPOLV--YTVNDNRC 184
DB 131 ISIDRYLAIVHATNSQ--KPKRLAEKVVYGVWIPALLTIPDFIFANVSEADRY 187
QY 185 IPFPYLGTSKALIQMLEICIGFVVPFLMGVCYFITARLMMKPNKISRPLKVLTT 244
DB 188 DREYPSDL--WLVFQFQHIWGLIPGILSCYCIISKLSHSGYQRRKALKTTVI 244
QY 245 VLVFVTOLPYNIYVFCRAIDYISLITSCNMSKRMIDIAIOVTSIALFHSCLPILYV 304
DB 245 LITTFACMLPYIIGISIDSFILEITIKOGCEFEFTVHKWISITETALAFHCCLPILYA 304
QY 305 FMGASFK 311
DB 305 FLGAKFK 311

Search completed: March 14, 2003, 16:12:36
Job time: 20 secs



Mon Mar 17 12:24:54 2003

us-09-686-020a-2.rag

Page 1

GenCore version 5.1.4-P5.4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 16:07:18 ; Search time 36 Seconds
(without alignments)
1295,492 Million cell updates/sec

Title: US-09-686-020A-2

Perfect score: 1819
Sequence: 1 MAFQNSTDYTYEENMNG.....VEEPPFDEGPTPTSTFTST 350

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A-Geneseq.101002.*
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|------------------------------|
| 1 | 1819 | 100.0 | 350 | 20 | AAV57290 Human BGCR protein |
| 2 | 1819 | 100.0 | 350 | 20 | AAV17435 Human signal peptid |
| 3 | 1819 | 100.0 | 350 | 20 | AAW93169 Human HETAO41 prot |
| 4 | 1819 | 100.0 | 350 | 21 | AAV94325 Human seven transm |
| 5 | 1819 | 100.0 | 350 | 22 | AAV80119 Human CCR1 protel |
| 6 | 1819 | 100.0 | 350 | 22 | AAV08994 Human G protein co |
| 7 | 1819 | 100.0 | 350 | 22 | AAV67237 Amino acid sequenc |
| 8 | 1819 | 100.0 | 382 | 22 | AAV62389 Human chemokine re |
| 9 | 1814 | 99.7 | 349 | 20 | AAW93170 Human HETAO41 prot |
| 10 | 1814 | 99.7 | 350 | 20 | AAV30125 A human seven-pass |

| | | | | | |
|----|------|------|-----|----|-------------------------------|
| 11 | 1810 | 99.5 | 350 | 21 | AAV71301 Human orphan G pro |
| 12 | 1810 | 99.5 | 350 | 21 | AAV82835 Human G protein co |
| 13 | 1808 | 99.4 | 350 | 20 | AAV37688 Human TSC7. Homo |
| 14 | 1728 | 95.0 | 333 | 20 | AAV57289 Human BGCR partia |
| 15 | 1620 | 89.1 | 350 | 22 | AAV67238 Amino acid sequenc |
| 16 | 1591 | 87.5 | 350 | 20 | AAV57291 Mouse BGCR protel |
| 17 | 1275 | 70.1 | 245 | 20 | AAV57292 Human BGCR protel |
| 18 | 1257 | 69.1 | 242 | 22 | AAV99949 Human expressed po |
| 19 | 1212 | 66.6 | 263 | 20 | AAV30126 A seven-pass trans |
| 20 | 862 | 47.4 | 164 | 22 | ABV11162 Human orphan GPCR |
| 21 | 824 | 45.3 | 159 | 21 | AAV41786 Human ORFX ORF150 |
| 22 | 761 | 41.8 | 175 | 22 | AAV87280 Human CDNA SRO ID |
| 23 | 761 | 41.8 | 175 | 22 | AAV99976 Human expressed po |
| 24 | 761 | 41.8 | 175 | 22 | ABV10276 Human endocrine po |
| 25 | 761 | 41.8 | 175 | 22 | AAV18115 Human central nerv |
| 26 | 761 | 41.8 | 175 | 22 | AAV18361 Human ORFX ORF150 |
| 27 | 761 | 41.8 | 175 | 22 | AAV18659 Renal and cardiopa |
| 28 | 761 | 41.8 | 175 | 22 | AAV21655 Partial human neopla |
| 29 | 659 | 36.2 | 358 | 15 | AAV53745 Human 7TM receptor |
| 30 | 659 | 36.2 | 358 | 23 | AAV48724 Human 7TM receptor |
| 31 | 659 | 36.2 | 358 | 21 | AAV91231 Human V31 seven tr |
| 32 | 659 | 36.2 | 378 | 19 | AAV21688 Human 7TM receptor |
| 33 | 659 | 36.2 | 378 | 22 | AAV80114 Human CCR7. Homo |
| 34 | 659 | 36.2 | 378 | 22 | AAV50859 Human 7 transmembr |
| 35 | 659 | 36.2 | 378 | 21 | AAV91230 Putative seven tra |
| 36 | 659 | 36.2 | 378 | 21 | AAV53743 Polypeptide sequen |
| 37 | 659 | 36.2 | 410 | 15 | AAV8723 Human 7 transmembr |
| 38 | 659 | 36.2 | 410 | 19 | AAV21687 Genomic clone of 7 |
| 39 | 659 | 36.2 | 410 | 21 | AAV91229 Human 7 transmembr |
| 40 | 659 | 36.2 | 410 | 23 | AAV91229 Novel human diagno |
| 41 | 659 | 36.2 | 569 | 22 | ABG1373 Putative seven tra |
| 42 | 659 | 36.2 | 378 | 15 | AAV53744 Human mutant G pro |
| 43 | 656 | 36.0 | 378 | 21 | AAV90663 Human G protein-co |
| 44 | 655 | 35.9 | 378 | 21 | AAV90662 |
| 45 | 653 | 35.9 | 378 | 21 | AAV90629 |

ALIGNMENTS

| | | |
|----------|--|----------------------------|
| RESULT 1 | AAV57290 | standard; Protein: 350 AA. |
| ID | AAV57290 | |
| XX | AAV57290 | |
| AC | 05-JUN-2000 | (first entry) |
| XX | | |
| DT | Human BGCR protein. | |
| DE | | |
| XX | BGCR protein: G-protein coupled receptor; human; chemokine; exocytosis; | |
| KW | cell proliferation; anti-inflammatory; anti-angiogenic; anticancer; HIV; | |
| KW | anti-allergic; antiviral. | |
| XX | | |
| OS | Homo sapiens. | |
| XX | | |
| PN | W09952945-A2. | |
| XX | | |
| PD | 21-OCT-1999. | |
| XX | | |
| PF | 16-APR-1999; | 99NO-US08395. |
| XX | | |
| PR | 16-APR-1998; | 98US-0061753. |
| XX | | |
| PR | 16-APR-1999; | 99US-0061753. |
| XX | | |
| PA | (MILL-) MILLENIUM PHARM INC. | |
| PI | Gonzalo JA, Gutierrez-Ramos JC; | |
| XX | | |
| DR | WPI: 1999-620375/53. | |
| XX | N-PDB: AA290528. | |
| PT | New nucleic acid encoding human BGCR receptor, used e.g. for | |

PT modulating inflammation and tumor growth
 PS Claim 8; Fig 2A-B; 123pp; English.
 XX

CC The invention relates to a human BGCR protein, a G-protein coupled
 CC receptor. The BGCR protein can be expressed by standard recombinant
 CC methodology. BGCR are receptor proteins possibly involved in modulation
 CC of proinflammatory or stimulatory functions of chemokines; cell
 CC proliferation, migration, adhesion and targeting; and exocytosis. The
 CC BGCR nucleic acids and derived proteins (or their variants), antibodies
 CC and modulators are potentially useful for modulating inflammation;
 CC chemotactic activity of leucocytes; angiogenesis; cell proliferation;
 CC tumor growth; allergic reactions and entry of human immune deficiency
 CC virus into cells, for therapeutic or prophylactic purposes. They are also
 CC used for diagnosis and in drug-screening assays. The present sequence
 CC represents the full-length human BGCR protein.
 XX

Sequence 350 AA:

Query Match Best Local Similarity 100.0%; Score 1819; DB 20; Length 350;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 M A L E D N O S T D Y Y E E N E M N G T Y D Y S O Y E L I C I K E D V R E F A K Y L P V F L T I V F V I G L A G N S 60
 DB 1 M A L E D N O S T D Y Y E E N E M N G T Y D Y S O Y E L I C I K E D V R E F A K Y L P V F L T I V F V I G L A G N S 60
 OY 61 M V V A I Y A Y Y K K O R T K D V Y L T L N A V A D L L L F T L P F M A V N A H G V L K I M C K I T S A L Y T 120
 DB 61 M V V A I Y A Y Y K K O R T K D V Y L T L N A V A D L L L F T L P F M A V N A H G V L K I M C K I T S A L Y T 120
 OY 121 L N F V S G M O F L A C I S I D R Y A V A T K V P S O S G V G K P C W I I C F C W M A A I L L S I P O L V F Y T V N D 180
 DB 121 L N F V S G M O F L A C I S I D R Y A V A T K V P S O S G V G K P C W I I C F C W M A A I L L S I P O L V F Y T V N D 180
 OY 181 N A R C I P F P R Y L G T S M K A L I O M L E T I C I G F V V P F L I M G C Y F I T A R T L M K P N I K I S R P L K 240
 DB 181 N A R C I P F P R Y L G T S M K A L I O M L E T I C I G F V V P F L I M G C Y F I T A R T L M K P N I K I S R P L K 240
 OY 241 V L T T V I V I F Y T Q L P Y N I V K F C R A I D I I Y S L I T S C N N S K R M D I A I O V T S I A L F H S C L N P 300
 DB 241 V L T T V I V I F Y T Q L P Y N I V K F C R A I D I I Y S L I T S C N N S K R M D I A I O V T S I A L F H S C L N P 300
 OY 301 I L Y V F M G A S F K N Y V M K A K K Y G S W R R O S V E E F P D S G P T E P T S T F S I 350
 DB 301 I L Y V F M G A S F K N Y V M K A K K Y G S W R R O S V E E F P D S G P T E P T S T F S I 350

RESULT 2

ID AAY17435 standard; Protein: 350 AA.
 AC AAY17435;
 XX

DT 29-JUL-1999 (first entry)
 XX

DE Human signal peptide-containing protein SP-16.
 XX

KW Human; signal peptide-containing protein: SP; cell proliferation;
 KW cancer; neuronal disorder; immune response; detection.
 XX

OS Homo sapiens.
 XX

PN WO9924463-A2.
 XX

PD 20-MAY-1999.
 XX

PF 04-NOV-1998; 98MO-US23578.
 XX

PR 07-NOV-1997; 97US-0966316.
 XX

PA (INCYT-) INCYTE PHARM INC.
 XX

PI Au-Young J, Lal P, Mathur P, Murry LE, Reddy R;
 XX WPI: 1999-337694/28.
 DR N-PSDB: AAX61288.
 XX

PT CDNA clones encoding signal peptide-containing proteins
 PS Claim 1; Fig 1; 83pp; English.
 XX

CC The present sequence represents a human signal peptide-containing
 CC protein (SP), designated SP-16. SP proteins can be used to stimulate
 CC cell proliferation or to treat or prevent cancer. SP antagonists are
 CC also used to treat or prevent cancer, and also for treating or
 CC preventing neuronal disorders or immune responses. Polynucleotide
 CC sequences complementary to the SP-encoding polynucleotides are useful
 CC for the detection of SP-encoding nucleic acid molecules in biological
 CC samples.
 XX

Sequence 350 AA:

Query Match Best Local Similarity 100.0%; Score 1819; DB 20; Length 350;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 M A L E D N O S T D Y Y E E N E M N G T Y D Y S O Y E L I C I K E D V R E F A K Y L P V F L T I V F V I G L A G N S 60
 DB 1 M A L E D N O S T D Y Y E E N E M N G T Y D Y S O Y E L I C I K E D V R E F A K Y L P V F L T I V F V I G L A G N S 60
 OY 61 M V V A I Y A Y Y K K O R T K D V Y L T L N A V A D L L L F T L P F M A V N A H G V L K I M C K I T S A L Y T 120
 DB 61 M V V A I Y A Y Y K K O R T K D V Y L T L N A V A D L L L F T L P F M A V N A H G V L K I M C K I T S A L Y T 120
 OY 121 L N F V S G M O F L A C I S I D R Y A V A T K V P S O S G V G K P C W I I C F C W M A A I L L S I P O L V F Y T V N D 180
 DB 121 L N F V S G M O F L A C I S I D R Y A V A T K V P S O S G V G K P C W I I C F C W M A A I L L S I P O L V F Y T V N D 180
 OY 181 N A R C I P F P R Y L G T S M K A L I O M L E T I C I G F V V P F L I M G C Y F I T A R T L M K P N I K I S R P L K 240
 DB 181 N A R C I P F P R Y L G T S M K A L I O M L E T I C I G F V V P F L I M G C Y F I T A R T L M K P N I K I S R P L K 240
 OY 241 V L T T V I V I F Y T Q L P Y N I V K F C R A I D I I Y S L I T S C N N S K R M D I A I O V T S I A L F H S C L N P 300
 DB 241 V L T T V I V I F Y T Q L P Y N I V K F C R A I D I I Y S L I T S C N N S K R M D I A I O V T S I A L F H S C L N P 300
 OY 301 I L Y V F M G A S F K N Y V M K A K K Y G S W R R O S V E E F P D S G P T E P T S T F S I 350
 DB 301 I L Y V F M G A S F K N Y V M K A K K Y G S W R R O S V E E F P D S G P T E P T S T F S I 350

RESULT 3

ID AAW93169 standard; Protein: 350 AA.
 AC AAW93169;
 XX

DT 24-MAY-1999 (first entry)
 XX

DE Human HPIA041 protein.
 XX

KW HPIA041; G-coupled receptor; disease susceptibility; diagnosis; immunise;
 KW treatment; HPIA041 protein; gene therapy; immune response; vaccine; HIV-2;
 KW inoculate; bacterial; fungal; protozoan; viral; infection; HIV-1; cancer;
 KW diabetes; anorexia; bulimia; Parkinson's disease; acute heart failure;
 KW hypotension; hypertension; urinary retention; osteoporosis; allergy;
 KW benign prostatic hyperplasia; myocardial infarction; ulcer; asthma; schizophrenia;
 KW anxiety; manic depression; psychosis; neurological disorder;
 KW dyslexia; Huntington's disease; Gilles de la Tourette's syndrome;
 KW linkage analysis; gene mapping; human.
 XX

OS Homo sapiens.
 XX

PN EP899332-A2.
 XX

Db 301 ILIVFMGASFKNYMKVAKKYGSWRQRQSVVEEFPDSEGTPTSTFSI 350

AA WPI; 1999-144803/13.
DR N-PSDB; AAX22557.
DR

XX New G-coupled receptor (HTR4041) polypeptide and polynucleotide
XX useful as diagnostic reagents and for prevention and treatment of
PT cancer, HIV infections and Parkinson's disease
PT
XX
XX claim 1, page 22-23; 27pp; English.

PS Claim 1: page 22
 XX This sequence represents a G-coupled receptor, HPIRA01 which is useful
 CC for diagnosing susceptibility to diseases by detecting mutations in the
 CC HPIRA01 gene, and can diagnose diseases associated with HPIRA01 proteins
 CC HPIRA01 gene, and can diagnose diseases associated with HPIRA01 proteins
 CC imbalance by determining HPIRA01 polypeptide expression levels. Agonists
 CC and antagonists of the protein can be used in treatment to activate
 CC (agonist) or inhibit (antagonist) HPIRA01 activity, in addition to direct
 CC administration of antisense sequences to prevent expression of HPIRA01
 CC polynucleotides to treat conditions associated with a lack of HPIRA01
 CC protein. Gene therapy may also be used to affect endogenous HPIRA01
 CC polypeptide expression. HPIRA01 antibodies are useful for inducing an
 CC immune response to immunize and prevent disease, and for isolating
 CC HPIRA01 clones or purifying the polypeptides by affinity chromatography.
 CC HPIRA01 polypeptides can be administered directly or as a vaccine to
 CC inoculate against disease. Diseases diagnosed, prevented and treated
 CC include bacterial, fungal, protozoan and viral infections, particularly
 CC HIV-1 or 2 infections; cancer; diabetes; anorexia; bulimia; Parkinson's
 CC disease; acute heart failure; hypotension; myocardial infarction; ulcers;
 CC retention; osteoporosis; angina pectoris; and psychotic and
 CC asthma; allergies; benign prostatic hypertrophy; and manic
 CC neurological disorders, including anxiety, schizophrenia, and dyskinetias
 CC depression, delirium, dementia, severe mental retardation and
 CC such as Huntington's disease or Gilles de la Tourette's syndrome. The
 CC HPIRA01 polypeptide is also useful for mapping the gene to a chromosome,
 CC allowing gene inheritance to be studied through linkage analysis.
 CC
 XX Sequence 350 AA:
 SQ

| Sequence | 350 AA: | Score | 1819: | DB | 20: | Length | 350: |
|-----------------------|---|-------|---------------|----|--------|--------|------|
| Query Match | 100.0%; | Pred | No. 1.9e-195; | | | | |
| Best Local Similarity | 100.0%; | | | | | | |
| Matches | Conservative | 0; | Mismatches | 0; | Indels | 0; | Gaps |
| QY | 1 MALEONOSRDYEEENENMGTYDSOYELICIEDYREFRAKFLPEVPLTIVFVIGLAGNS 60 | | | | | | |
| Db | 1 MALEONOSRDYEEENENMGTYDSOYELICIEDYREFRAKFLPEVPLTIVFVIGLAGNS 60 | | | | | | |
| QY | 61 MVAIAYYYKKQKRTKDYIILNLAVADLLLEFLPEVAANAHVGLGIMCKITSALT 120 | | | | | | |
| Db | 61 MVAIAYYYKKQKRTKDYIILNLAVADLLLEFLPEVAANAHVGLGIMCKITSALT 120 | | | | | | |
| QY | 61 MVAIAYYYKKQKRTKDYIILNLAVADLLLEFLPEVAANAHVGLGIMCKITSALT 120 | | | | | | |
| Db | 61 MVAIAYYYKKQKRTKDYIILNLAVADLLLEFLPEVAANAHVGLGIMCKITSALT 120 | | | | | | |
| QY | 121 LNFVSGMQLACISIDRYAVATKVPSSQGVKPCMCICFCVMAAAILSTPOLVFTYND 180 | | | | | | |
| Db | 121 LNFVSGMQLACISIDRYAVATKVPSSQGVKPCMCICFCVMAAAILSTPOLVFTYND 180 | | | | | | |
| QY | 181 NARCIPEPRPLVLSMKALLQMLEICIGFVPEPLMGVCYFTTARTLTKMKRNKISRPK 240 | | | | | | |
| Db | 181 NARCIPEPRPLVLSMKALLQMLEICIGFVPEPLMGVCYFTTARTLTKMKRNKISRPK 240 | | | | | | |
| QY | 241 VLLTVAVIVETQLPYNTVYKFCRAIDIIYSLTSCNMSKRMADIAQTVESTALFHSCLNP 300 | | | | | | |
| Db | 241 VLLTVAVIVETQLPYNTVYKFCRAIDIIYSLTSCNMSKRMADIAQTVESTALFHSCLNP 300 | | | | | | |
| QY | 301 ILTVFVGASFKYVYMKVAKKYGSMRROKOSVEEFPFDSGPEPTSTPS 350 | | | | | | |
| Db | 301 ILTVFVGASFKYVYMKVAKKYGSMRROKOSVEEFPFDSGPEPTSTPS 350 | | | | | | |

301 ILYVEMGASL AND VANDER...

RESULT 4
AAV94325 standard; Protein; 350 AA

AA94325; AC

11-AUG-2000 (first entry)

Human seven transmembrane receptor

Homo sapiens

| XX | Location/Qualifiers |
|----|---------------------|
| XX | |

| | | |
|---------------|--------|---------------------------------|
| En | 6.8 | |
| Modified-site | | "potential N-glycosylation site |
| FT | /note= | |

| FT | Modified-site | 19..21 | "potential N-glycosyl |
|----|---------------|--------|-----------------------|
| FT | | /note= | |

| FTT | 42..66 |
|--------|----------------------|
| FT | Transmembrane_domain |
| Domain | label= |

| Domain | Transmembrane_domain |
|--------|----------------------|
| FT | 79..100 |
| FT | 1..100 |

| Domain | 135 |
|--------|----------|
| FT | 114..135 |
| FT | 114..135 |

| Domain | FT | FT |
|----------------------|----------|----|
| transmembrane domain | 156..175 | |

FT 199. . 221

241.:262 /label= domain

276..278

```

E1      /note="potencial" n="3"
FT      287..308

```

Don't know
FT
FT
/label= Transmembrane domain

XX
PN
WO200026369-A1.

XX
PD
11-MAY-2000.

XX 99WO-US25848.
DE 03-NOV-1999;

XX 98US-0107112.
00-NOV-1998;
XX

PR 06-JAN-1999; 9905-0114800.

AA
PA (CHIR) CHIRON CORP.

XX Shymala V;
PI khoja H;

XX
DR
WPI: 2000-365618/31.

DR N-PSDB; AAL 300000
XX

Novel polypeptides containing
and its encoding polynucleotide, useful

XX
XX
Claim 3: Fig 1; 79pp; English.

sequence is VSHK-1, a new ser-

receptor which contains seven membrane-linked by three intracellular an

CC gene sequence encoding VSHK-1 was isolated
CC from a cDNA library and was predominantly found
CC in the testis.

CC tissue, where
CC identified: a
CC sequence correspond

CC encoding the presence of an alternative exon at a nucleotide position. CC form may result from the use of an alternative intron at a nucleotide position.

transcription of a 5'-
CC transcription of a 5'-
CC transcription of a 5'-
5 0kb species. VSHK-1 polynucleotides ca

to detect and measure VSNs. These substances that modulate the level of VSNs

1

sequence can be integrated into an expression vector for production of VSHK-1 receptor polypeptides in host cells. The polypeptides can be used to identify agents which modulate VSHK-1 receptor signal transduction activity.

Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 21; Length 350; Best Local Similarity 100.0%; Pred. No. 1.9e-195; Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MALEONOSTDYEEENKNGTYDYSQYELICIKEDVREFAKFLPVLITVFIAGLNS 60
 1 MALEONOSTDYEEENKNGTYDYSQYELICIKEDVREFAKFLPVLITVFIAGLNS 60
 61 MVVAIYAYKKKRTKTDVYILNLAADLLFTLPFMAVNAHGVGKIMCKTTSALT 120
 61 MVVAIYAYKKKRTKTDVYILNLAADLLFTLPFMAVNAHGVGKIMCKTTSALT 120
 121 LNFVSGMOFLACISIDRYVAATKVPSSGSGKPCWIIICFCVMAAILLSTPOLVFTVND 180
 121 LNFVSGMOFLACISIDRYVAATKVPSSGSGKPCWIIICFCVMAAILLSTPOLVFTVND 180
 181 NARCIPIFRYIGTSMKALIQMLEICIGFVVPFLIMGVCYFIARTLMKMPNIKISRPLK 240
 181 NARCIPIFRYIGTSMKALIQMLEICIGFVVPFLIMGVCYFIARTLMKMPNIKISRPLK 240
 241 VLTAVIVIVTQLPYINIVKFCRAIDITISLITSCNMSKRMIDIAIQVETSIALPHSCLNP 300
 241 VLTAVIVIVTQLPYINIVKFCRAIDITISLITSCNMSKRMIDIAIQVETSIALPHSCLNP 300
 301 ILIYVMSGASFKNYVAKKYGSMRQROSVBEPPDSGEPTEPTSTFSI 350
 301 ILIYVMSGASFKNYVAKKYGSMRQROSVBEPPDSGEPTEPTSTFSI 350

RESULT 5

AAG80119 standard; Protein: 350 AA.

AAG80119; 17-JAN-2002 (first entry)
 Human CCR1 protein.
 Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection; inflammation; autoimmune disease; metastasis; bronchial asthma; lupus; chronic bowel inflammation; rheumatoid arthritis; cytostatic; antineoplastic; antiarthritic; immunosuppressive; dermatological; antineoplastic; antiarthritic.

Homo sapiens.
 WO200172830-A2.
 04-OCT-2001.
 02-APR-2001: 2001WO-EP03708.
 31-MAR-2000: 2000DE-1016013.
 (IPF-) IPF PHARM GMBH.
 (FORS/) FORSMANN U.
 Forssmann W, Adermann K, Heitland A, Spodsberg N;
 WPI: 2001-626256/72.
 Diagnostic agent containing two or more receptor-specific ligands, useful for detecting tumors, inflammation etc., also therapeutic use of ligand inhibitors

PS Disclosure; Page 11; 26pp; German.

CC This invention describes a novel diagnostic agent (A) comprising at least two different ligands (I) for receptors (II) that are implicated in disease (A) are used for the diagnosis of tumors (especially colorectal or prostatic), organ rejection, inflammation and autoimmune diseases. Also inhibitors of (I) are used therapeutically against tumors (and their metastases), inflammation (particularly bronchial asthma or chronic bowel inflammation), or autoimmune diseases (rheumatoid arthritis or lupus) where the (cardio)vascular, lymphatic, respiratory, nervous, digestive, endocrine, motor or urogenital systems or skin are affected, and bone marrow diseases. The products of the invention are chemokine derivatives which have cytostatic, antiinflammatory, antineoplastic, antitumor, immunosuppressive, dermatological, antineoplastic, antitumor, chemokines act on specific tumor and inflammatory cells through a proliferation of these cells. AAG80045-AAG80128 represent human chemokine fragments used to illustrate the method of the invention.

Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 22; Length 350; Best Local Similarity 100.0%; Pred. No. 1.9e-195; Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MALEONOSTDYEEENKNGTYDYSQYELICIKEDVREFAKFLPVLITVFIAGLNS 60
 1 MALEONOSTDYEEENKNGTYDYSQYELICIKEDVREFAKFLPVLITVFIAGLNS 60
 61 MVVAIYAYKKKRTKTDVYILNLAADLLFTLPFMAVNAHGVGKIMCKTTSALT 120
 61 MVVAIYAYKKKRTKTDVYILNLAADLLFTLPFMAVNAHGVGKIMCKTTSALT 120
 121 LNFVSGMOFLACISIDRYVAATKVPSSGSGKPCWIIICFCVMAAILLSTPOLVFTVND 180
 121 LNFVSGMOFLACISIDRYVAATKVPSSGSGKPCWIIICFCVMAAILLSTPOLVFTVND 180
 181 NARCIPIFRYIGTSMKALIQMLEICIGFVVPFLIMGVCYFIARTLMKMPNIKISRPLK 240
 181 NARCIPIFRYIGTSMKALIQMLEICIGFVVPFLIMGVCYFIARTLMKMPNIKISRPLK 240
 241 VLTAVIVIVTQLPYINIVKFCRAIDITISLITSCNMSKRMIDIAIQVETSIALPHSCLNP 300
 241 VLTAVIVIVTQLPYINIVKFCRAIDITISLITSCNMSKRMIDIAIQVETSIALPHSCLNP 300
 301 ILIYVMSGASFKNYVAKKYGSMRQROSVBEPPDSGEPTEPTSTFSI 350
 301 ILIYVMSGASFKNYVAKKYGSMRQROSVBEPPDSGEPTEPTSTFSI 350

RESULT 6

AAU08994 standard; Protein: 350 AA.

AAU08994; 18-DEC-2001 (first entry)
 Human G protein-coupled receptor, GPCR, 2398.
 Human; GPCR; G protein-coupled receptor; 2398; cardiant; antithrombotic; analgesic; cytoskeletal; angiogenic; cardiovascular disorder; pain response disorder; inflammatory disorder; atherosclerosis; angina pectoris; myocardial infarction; hypertensive heart disease; sudden cardiac death; obesity; hypertension; diabetes; prostate cancer-related pain.

Key Location/Qualifiers
 125..141
 Region /Label= G-protein_receptor_signature

XX
PN WO200164882-A2.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US06543.
XX
PR 29-FEB-2000; 2000US-186059P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Glucksmann MA, Galvin KM, Slios-Santiago I;
XX
DR WPI; 2001-589866/56.
XX
DR N-PSDB; AAS14572.
XX
PT Novel G protein coupled receptors and nucleic acids encoding them, for
PT identifying agents for the treatment of cardiac disorders
XX
PS Claim 9; Fig 9; 209pp; English.
XX
CC The invention relates to novel human G protein-coupled receptors (GPCR)
CC named 1983, 52881, 2398, 45449, 50289 and 52872. The novel GPCRs and
CC nucleic acids encoding them are useful for identifying agents for the
CC treatment of cardiovascular disorders, angiogenesis-related disorders,
CC neural disorders, pain response disorders and inflammatory disorders
CC e.g. atherosclerosis, angina pectoris and myocardial infarction,
CC ischemic heart disease, sudden cardiac death, hypertensive heart
CC disease, diabetes, prostate cancer-related pain, diabetes and obesity.
CC The present sequence represents GPCR 2398.
XX
SQ Sequence 350 AA:
XX
Query Match 100.0%; Score 1819; DB 22; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.9e-195;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MALEONOSTDYEEENEMNGTYDYSOYELICIKEDYREFAKVLPVFLTIVFVIGLAGNS 60
DB 1 MALEONOSTDYEEENEMNGTYDYSOYELICIKEDYREFAKVLPVFLTIVFVIGLAGNS 60
XX
QY 61 MVAATAYYKKORTDVTYILNLAVADLLFTLPFMANVAVHGVGLKIMCKTTSALYT 120
DB 61 MVAATAYYKKORTDVTYILNLAVADLLFTLPFMANVAVHGVGLKIMCKTTSALYT 120
XX
QY 121 LNFVSGMOFLACTSIDRYVAVTKVPSQSGVKGPCWIIICFCVMAAILLSIPOLVFYTVND 180
DB 121 LNFVSGMOFLACTSIDRYVAVTKVPSQSGVKGPCWIIICFCVMAAILLSIPOLVFYTVND 180
XX
QY 181 NARCIPIPRYLGTSKMAIOMLEICIGFVVPFLMGVCYFTARTLKMKNIRISPLK 240
DB 181 NARCIPIPRYLGTSKMAIOMLEICIGFVVPFLMGVCYFTARTLKMKNIRISPLK 240
XX
QY 241 VLTAVVIVFIVTQLPYNIIVKFCRAIDIIYSLITSCNMSKRDIAIOVTESTIALFHSCLP 300
DB 241 VLTAVVIVFIVTQLPYNIIVKFCRAIDIIYSLITSCNMSKRDIAIOVTESTIALFHSCLP 300
XX
QY 301 ILVYEMASRKNYVMKAKYKYSMBROBOSVEEFPDSGPTPESTPST 350
DB 301 ILVYEMASRKNYVMKAKYKYSMBROBOSVEEFPDSGPTPESTPST 350
XX
RESULT 7
ID AAG67237 standard; protein; 350 AA.
XX
AC AAG67237;
XX
DT 13-NOV-2001 (first entry)
XX
DE Amino acid sequence of human chemokine receptor CCR11.
XX
KW Human; chemokine receptor; CCR11; G protein coupled receptor;

KW inflammatory disease; rheumatoid arthritis; inflammatory bowel disease;
KW asthma; angiogenesis; atherosclerosis vascular association disease;
KW hypertension; angina pectoris; cardiac arrhythmia; Raynaud's phenomenon;
KW left ventricular diastolic dysfunction; migraine; preterm labour;
KW oesophageal spasm; ischemic stroke; subarachnoid haemorrhage;
KW myocardial infarction; congestive heart failure; endometriosi;
KW vasospasm; retinopathy; nephropathy; pulmonary vascular disease.
XX
OS Homo sapiens.
XX
PN WO200166598-A2.
XX
PD 13-SEP-2001.
XX
PF 05-MAR-2001; 2001WO-US07073.
XX
PR 03-MAR-2000; 2000US-0186928.
XX
PR 03-MAR-2000; 2000US-0187231.
XX
PA (ICOS-) ICOS CORP.
XX
PI Gray PM, Schmelckart VL, Epp A, Raport CJ, Chantry D, Steiner B;
XX
DR WPI; 2001-541918/60.
XX
DR N-PSDB; AAH77711.
XX
PT An isolated polynucleotide encoding the chemokine receptor CCR11,
PT useful for treating rheumatoid arthritis, inflammatory bowel disease,
PT asthma, angiogenesis, atherosclerosis, cardiac arrhythmias, Raynaud's
PT phenomenon and migraine -
XX
PS Claim 13; Page 96-97; 110pp; English.
XX
CC The present sequence represents the human chemokine receptor CCR11.
CC CCR11 is a member of the G protein coupled receptor family. A CCR11
CC polypeptide, its inhibitor, an antibody, or other modulator of CCR11
CC expression or biological activity, is useful for treating many
CC inflammatory diseases, for example, rheumatoid arthritis, inflammatory
CC bowel disease, and asthma. They are also useful for treating
CC angiogenesis, atherosclerosis vascular association diseases which may
CC include but are not limited to hypertension, angina pectoris, cardiac
CC arrhythmias, left ventricular diastolic dysfunction, Raynaud's
CC phenomenon, migraine, preterm labour, oesophageal spasm, ischemic
CC stroke, subarachnoid haemorrhage, myocardial infarction, congestive
CC heart failure, endometriosi, vasospasm, retinopathy, nephropathy, or
CC pulmonary vascular disease.
XX
SQ Sequence 350 AA:
XX
Query Match 100.0%; Score 1819; DB 22; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.9e-195;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MALEONOSTDYEEENEMNGTYDYSOYELICIKEDYREFAKVLPVFLTIVFVIGLAGNS 60
DB 1 MALEONOSTDYEEENEMNGTYDYSOYELICIKEDYREFAKVLPVFLTIVFVIGLAGNS 60
XX
QY 61 MVAATAYYKKORTDVTYILNLAVADLLFTLPFMANVAVHGVGLKIMCKTTSALYT 120
DB 61 MVAATAYYKKORTDVTYILNLAVADLLFTLPFMANVAVHGVGLKIMCKTTSALYT 120
XX
QY 121 LNFVSGMOFLACTSIDRYVAVTKVPSQSGVKGPCWIIICFCVMAAILLSIPOLVFYTVND 180
DB 121 LNFVSGMOFLACTSIDRYVAVTKVPSQSGVKGPCWIIICFCVMAAILLSIPOLVFYTVND 180
XX
QY 181 NARCIPIPRYLGTSKMAIOMLEICIGFVVPFLMGVCYFTARTLKMKNIRISPLK 240
DB 181 NARCIPIPRYLGTSKMAIOMLEICIGFVVPFLMGVCYFTARTLKMKNIRISPLK 240
XX
QY 241 VLTAVVIVFIVTQLPYNIIVKFCRAIDIIYSLITSCNMSKRDIAIOVTESTIALFHSCLP 300
DB 241 VLTAVVIVFIVTQLPYNIIVKFCRAIDIIYSLITSCNMSKRDIAIOVTESTIALFHSCLP 300

OY 301 ILVFMGASFKNYVMKVKYSGMROROSVEEFPDSEGPTEPTFSI 350
 DB 301 ILVFMGASFKNYVMKVKYSGMROROSVEEFPDSEGPTEPTFSI 350

RESULT 8 AAB62389

ID AAB62389 standard; protein; 382 AA.

AC AAB62389.

DT 29-JUN-2001 (first entry)

DE Human chemokine receptor CCX CKR polypeptide.

KW Chemokine receptor; CCX CKR; chemokine; ELC; SLC; TECK; modulator;
 KW antiinflammatory; immunosuppressive; cytostatic; antiallergic; human;
 KW immunostimulant; gene therapy.

OS Homo sapiens.

PH Key Location/Qualifiers

FT Misc-difference 351 /note= "encoded by TAA"

FT Misc-difference 353 /note= "encoded by TAA"

FT Misc-difference 365 /note= "encoded by TGA"

FT Misc-difference 371 /note= "encoded by TAA"

PN WO200127146-A2.

PD 19-APR-2001.

PF 10-OCT-2000: 2000WO-US28067.

XX 12-OCT-1999: 99US-0159015.

PR 13-OCT-1999: 99US-0159210.

PR 20-DEC-1999: 99US-0172979.

PR 28-DEC-1999: 99US-0173389.

PR 03-MAR-2000: 2000US-0186626.

PA (CHEM-) CHEMOCENTRIX INC.

PI Gosling J, Dairaghi DJ, Hanley M, Miao Z, Talbot D, Schall TJ;

XX WPI: 2001-281975/29.

DR N-PSDB: AAF57685.

XX Isolated or recombinant chemokine receptor (designated CCX CKR)

PT polypeptide (PI) or its fragment, useful for identifying CCX CKR

PT modulators which can be used in the treatment of inflammation, allergy,

PT an autoimmune disease or cancer -

XX Claim 4; Fig 1; 72pp; English.

XX The invention relates to an isolated or recombinant chemokine receptor

CC designated CCX CKR) polypeptide which binds to chemokines such as ELC,

CC SLC or TECK. The CCX CKR polypeptide is useful for identifying CCX CKR

CC modulators. An agent that modulates the activity or expression of CCX CKR

CC in a cell or tissue in the mammal is useful in the treatment of a CCX CKR

CC -mediated condition such as inflammation, allergy, an autoimmune disease,

CC graft rejection, cancer, an infectious disease or an immunosuppressive

CC disease. The present sequence represents the human CCX CKR polypeptide.

XX Sequence 382 AA:

Query Match 100.0%; Score 1819; DB 22; Length 382;

Best Local Similarity 100.0%; Pred. No. 2.2e-195;

Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MALEONOSTDYEEENENGTYYDSQYELICIKEDVREFAKVLPVFLTIVFVIGLAGNS 60

DB 1 MALEONOSTDYEEENENGTYYDSQYELICIKEDVREFAKVLPVFLTIVFVIGLAGNS 60
 OY 61 NVVAIYAYKKKORTKTDYIILNLAVALLLFTLPFMAVNAVHGVLGKIMCKITSLALT 120
 DB 61 NVVAIYAYKKKORTKTDYIILNLAVALLLFTLPFMAVNAVHGVLGKIMCKITSLALT 120
 OY 121 LNFVSGMOFLACISIDRVAAVATKVPSSGSGVKPCMIICFCVMAAILLSTPOLVFYVND 180
 DB 121 LNFVSGMOFLACISIDRVAAVATKVPSSGSGVKPCMIICFCVMAAILLSTPOLVFYVND 180
 OY 181 NARCIPFPRYLGTSMAKLIOMLEICIGFVVPFLMGCVETARTLMKMPNIRSLK 240
 DB 181 NARCIPFPRYLGTSMAKLIOMLEICIGFVVPFLMGCVETARTLMKMPNIRSLK 240
 OY 241 VLLTVVYFVITQLPYNNVVKFCRAIDITYSLITSCNMSKRDIAIOYTESIALFHSCLNP 300
 DB 241 VLLTVVYFVITQLPYNNVVKFCRAIDITYSLITSCNMSKRDIAIOYTESIALFHSCLNP 300
 OY 301 ILVFMGASFKNYVMKVKYSGMROROSVEEFPDSEGPTEPTFSI 350
 DB 301 ILVFMGASFKNYVMKVKYSGMROROSVEEFPDSEGPTEPTFSI 350

RESULT 9

AAW93170 standard; protein; 349 AA.

AAW93170:

DT 24-MAY-1999 (first entry)

XX Human HF1A04 protein.

DE HF1A04: G-coupled receptor; disease susceptibility; diagnosis; immunise;

KW treatment; F1A041 protein; gene therapy; immune response; vaccine; HIV-2;

KW inoculate; bacterial; fungal; protozoan; viral; infection; HIV-1; cancer;

KW diabetes; anorexia; bulimia; Parkinson's disease; acute heart failure;

KW hypotension; hypertension; urinary retention; osteoporosis; allergy;

KW angina pectoris; myocardial infarction; ulcer; asthma; schizophrenia;

KW benign prostatic hypertrophy; psychotic disorder; neurological disorder;

KW anxiety; manic depression; delirium; dementia; severe mental retardation;

KW dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome;

KW linkage analysis; gene mapping; human; ss.

OS Homo sapiens.

XX EP699332-A2.

PN 03-MAR-1999.

PD 17-FEB-1998: 98EP-0301170.

XX 27-OCT-1997: 97US-0962922.

PR 15-AUG-1997: 97US-0055895.

XX (SMK) SMITHKLINE BEECHAM CORP.

XX E1115 CE;

XX WPI: 1999-144803/13.

DR N-PSDB: AAX22558.

XX New G-coupled receptor (HF1A041) polypeptide and polynucleotide -

PT useful as diagnostic reagents and for prevention and treatment of

PT cancer, HIV infections and Parkinson's disease

XX Disclousure: Page 25-26; 27pp; English.

XX This sequence encodes a G-coupled receptor, HF1A041 which is useful for

CC diagnosing susceptibility to diseases by detecting mutations in the

CC HF1A041 gene, and can diagnose diseases associated with HF1A041 protein

CC imbalance by determining HF1A041 polypeptide expression levels. Agonists

CC and antagonists of the protein can be used in treatment to activate
CC (agonist) or inhibit (antagonist) Hf1A041 activity. In addition to direct
CC administration of antisense sequences to prevent expression, or Hf1A041
CC polynucleotides to treat conditions associated with a lack of Hf1A041
CC protein. Gene therapy may also be used to affect endogenous Hf1A041
CC polypeptide expression. Hf1A041 antibodies are useful for inducing an
CC immune response to immunise and prevent disease, and for isolating
CC Hf1A041 clones or purifying the polypeptides by affinity chromatography.
CC Hf1A041 polypeptides can be administered directly or as a vaccine to
CC inoculate against disease. Diseases diagnosed, prevented and treated
CC include bacterial, fungal, protozoan and viral infections, particularly
CC HIV-1 or -2 infections; cancer; diabetes; anorexia; bulimia; Parkinson's
CC disease; acute heart failure; hypotension; hypertension; urinary
CC retention; osteoporosis; angina pectoris; myocardial infarction; ulcers;
CC asthma; allergies; benign prostatic hypertrophy; and psychotic and
CC neurological disorders, including anxiety, schizophrenia, manic
CC depression, delirium, dementia, severe mental retardation and dyskinesias
CC such as Huntington's disease or Gilles de la Tourette's syndrome. The
CC Hf1A041 polypeptide is also useful for mapping the gene to a chromosome,
CC allowing gene inheritance to be studied through linkage analysis.
XX

SQ Sequence 349 AA:

Query Match 99.7%; Score 1814; DB 20; Length 349;
Best Local Similarity 100.0%; Pred. No. 7e-195;
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ALEQNSTDYEEENMGNGTYDSQYELICIKEDVREFAKFLPVFLTFVFIAGLNSM 61
DB 1 ALEQNSTDYEEENMGNGTYDSQYELICIKEDVREFAKFLPVFLTFVFIAGLNSM 60
QY 62 VVAIVAYKKQRTKTDVYIILNLAVALDLLFTLPFWANAVHGWLGKIMCKITSAIYT 121
DB 61 VVAIVAYKKQRTKTDVYIILNLAVALDLLFTLPFWANAVHGWLGKIMCKITSAIYT 120
QY 122 NEFSGMOFLACISIDRVAVATKVPSSGSGVKPCWIIICFCVMAAILLSIPOLVFYTVND 181
DB 121 NEFSGMOFLACISIDRVAVATKVPSSGSGVKPCWIIICFCVMAAILLSIPOLVFYTVND 180
QY 182 ARCIPIFPRLGTSMAKALIQMLEICIGFVVPFLIMGVCFITARTLMKMPNIRKISPLK 241
DB 181 ARCIPIFPRLGTSMAKALIQMLEICIGFVVPFLIMGVCFITARTLMKMPNIRKISPLK 240
QY 242 LITVTVIYFTYQLPYNIVKFCRAIDITISLITSCNMSKRMIDIAIQTESIATLHSCINP 301
DB 241 LITVTVIYFTYQLPYNIVKFCRAIDITISLITSCNMSKRMIDIAIQTESIATLHSCINP 300
QY 302 LLYVMGASFKNYVMKAKKYGSMRROSYVEEPPDESGTPTSTFSI 350
DB 301 LLYVMGASFKNYVMKAKKYGSMRROSYVEEPPDESGTPTSTFSI 349

RESULT 10

AA30125

ID AAY30125 standard; Protein: 350 AA.

XX AC AAY30125;

DT 14-OCT-1999 (first entry)

DE A human seven-pass transmembrane receptor protein.

KW Seven-pass transmembrane receptor; autoimmune disease;

KM white blood cell dysfunction.

XX OS Homo sapiens.

XX PN WO9933876-A1.

XX PD 08-JUL-1999.

XX PF 24-DEC-1998; 98WO-JP05886.

XX

PR 24-DEC-1997; 97JP-0354537.
XX (ASAH) ASAH KASEI KOGYO KK.
XX Ishimaru H, Koshio T, Ohno T;
PI WPI: 1999-493806/41.
DR N-PSDB: AAX86674.
XX
PT New seven-pass transmembrane receptor protein useful for treating,
PT preventing or diagnosing autoimmune diseases
PS Claim 1: Page 101-103; 118pp; Japanese.
XX
XX The present sequence represents a seven-pass transmembrane receptor
CC protein. The protein and its DNA can be used to screen substances
CC for the diagnosis, prevention and treatment of autoimmune diseases,
CC particularly those due to white blood cell dysfunction.
XX

SQ Sequence 350 AA:

Query Match 99.7%; Score 1814; DB 20; Length 350;
Best Local Similarity 99.7%; Pred. No. 7e-195;
Matches 349; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEQNSTDYEEENMGNGTYDSQYELICIKEDVREFAKFLPVFLTFVFIAGLNS 60
DB 1 MALEQNSTDYEEENMGNGTYDSQYELICIKEDVREFAKFLPVFLTFVFIAGLNS 60
QY 61 MVAIVAYKKQRTKTDVYIILNLAVALDLLFTLPFWANAVHGWLGKIMCKITSAIYT 120
DB 61 MVAIVAYKKQRTKTDVYIILNLAVALDLLFTLPFWANAVHGWLGKIMCKITSAIYT 120
QY 121 LNFVSGMOFLACISIDRVAVATKVPSSGSGVKPCWIIICFCVMAAILLSIPOLVFYTVND 180
DB 121 LNFVSGMOFLACISIDRVAVATKVPSSGSGVKPCWIIICFCVMAAILLSIPOLVFYTVND 180
QY 181 NARCIPIFPRLGTSMAKALIQMLEICIGFVVPFLIMGVCFITARTLMKMPNIRKISPLK 240
DB 181 NARCIPIFPRLGTSMAKALIQMLEICIGFVVPFLIMGVCFITARTLMKMPNIRKISPLK 240
QY 241 VLTVTVIYFTYQLPYNIVKFCRAIDITISLITSCNMSKRMIDIAIQTESIATLHSCINP 300
DB 241 VLTVTVIYFTYQLPYNIVKFCRAIDITISLITSCNMSKRMIDIAIQTESIATLHSCINP 300
QY 301 LLYVMGASFKNYVMKAKKYGSMRROSYVEEPPDESGTPTSTFSI 350
DB 301 LLYVMGASFKNYVMKAKKYGSMRROSYVEEPPDESGTPTSTFSI 349

RESULT 11

AA71301

ID AAY71301 standard; Protein: 350 AA.

XX AC AAY71301;

DT 02-NOV-2000 (first entry)

DE Human orphan G protein-coupled receptor hppr1.

KW Human; orphan G protein-coupled receptor; GPCR; hppr1; drug screening;

KM transmembrane receptor; expressed sequence tag; EST; signal cascade.

XX OS Homo sapiens.

XX PN WO200031258-A2.

XX PD 02-JUN-2000.

XX PF 13-OCT-1999; 99WO-US23687.

XX PR 20-NOV-1998; 98US-0109213.

XX PR 16-FEB-1999; 99US-0120416.

XX

PR 26-FEB-1999; 99US-0121852.
 PR 12-MAR-1999; 99US-0123946.
 PR 12-MAR-1999; 99US-0123946.
 PR 28-MAY-1999; 99US-0136436.
 PR 28-MAY-1999; 99US-0136437.
 PR 28-MAY-1999; 99US-0136439.
 PR 28-MAY-1999; 99US-0136567.
 PR 28-MAY-1999; 99US-0137127.
 PR 28-MAY-1999; 99US-0137131.
 PR 29-JUN-1999; 99US-0141448.
 PR 29-SEP-1999; 99US-0156555.
 PR 29-SEP-1999; 99US-0156633.
 PR 29-SEP-1999; 99US-0156634.
 PR 29-SEP-1999; 99US-0156653.
 PR 01-OCT-1999; 99US-0157280.
 PR 01-OCT-1999; 99US-0157281.
 PR 01-OCT-1999; 99US-0157282.
 PR 01-OCT-1999; 99US-0157293.
 PR 01-OCT-1999; 99US-0157294.
 PR 12-OCT-1999; 99US-0416760.
 PR 12-OCT-1999; 99US-0417044.

XX (AREN-) ARENA PHARM INC.

PI Chen R, Dang HT, Liao CW, Lin I;

DR WPI; 2000-40068/34.

DR N-PSDB; AAD01128.

PT Novel human orphan G protein-coupled receptors and the encoding cDNAs
 for use in the identification of G protein-coupled receptor agonists -

PS Claim 42; Page 69-70; 102pp; English.

CC The present amino acid sequence is the hpprl, an endogenous human
 CC orphan G protein-coupled receptor (GPCR), expressed in the pituitary
 CC gland, heart, salivary gland, small intestine and testis. The hpprl cDNA
 CC was identified using EST (expressed sequence tag) AA35504 and 238667 as
 CC a probe. The orphan GPCR of the invention, like all GPCRs has seven
 CC transmembrane alpha helices with an extracellular N-terminus and an
 CC intracellular C-terminus. However, no endogenous ligands has yet been
 CC identified for the proteins of the invention. The orphan GPCRs may be
 CC used in the identification of their endogenous ligands, and to screen
 CC potential GPCR agonists and antagonists for use as pharmaceutical agents.
 CC The proteins may also be used in the study of GPCR-mediated signalling
 CC cascades, and to elucidate their precise role in normal and diseased
 CC human conditions. Nucleic acid encoding human orphan GPCRs may be used
 CC for tissue localisation expression analysis to provide information about
 CC their function in healthy and pathological states.

SQ Sequence 350 AA:

Query Match 99.5%; Score 1810; DB 21; Length 350;

Best Local Similarity 99.4%; Pred. No. 2e-194; Mismatches 2; Indels 0; Gaps 0;

Matches 348; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MALEQNSQSTDYEEENEMNGTIDYDQYELICIKEDVREFAKVLPVFLITVFIAGLNS 60
 DB 1 MALEQNSQSTDYEEENEMNGTIDYDQYELICIKEDVREFAKVLPVFLITVFIAGLNS 60
 QY 61 MVAIVAYVYKRRKRTDVTYILNLAVALDLLFTLPFAVAVAAGVGLKMTCTTALYT 120
 DB 61 MVAIVAYVYKRRKRTDVTYILNLAVALDLLFTLPFAVAVAAGVGLKMTCTTALYT 120
 QY 121 LNFVSGQFLACISIDRYAVATKVPSSGVKPCWIIICFCVMAAILLSIPOLVFTVND 180
 DB 121 LNFVSGQFLACISIDRYAVATKVPSSGVKPCWIIICFCVMAAILLSIPOLVFTVND 180
 QY 121 LNFVSGQFLACISIDRYAVATKVPSSGVKPCWIIICFCVMAAILLSIPOLVFTVND 180
 DB 121 LNFVSGQFLACISIDRYAVATKVPSSGVKPCWIIICFCVMAAILLSIPOLVFTVND 180
 QY 181 NARCIPIFPYRLGTSMKALIQMLEICIGFVPPPLMGVCYFTTARTLMKPNIKISRLK 240
 DB 181 NARCIPIFPYRLGTSMKALIQMLEICIGFVPPPLMGVCYFTTARTLMKPNIKISRLK 240
 QY 241 VLVTVIVFIVTQLPYIVAFCAIDITISLTSCNMSKMDIAIOVTESIALFHSCLNP 300

DB 241 VLVTVIVFIVTQLPYIVAFCAIDITISLTSCNMSKMDIAIOVTESIALFHSCLNP 300
 QY 301 ILYVFMGASFKNYVMKVKKGSWMROROSVEEPFDEGTEPTSPSI 350
 DB 301 ILYVFMGASFKNYVMKVKKGSWMROROSVEEPFDEGTEPTSPSI 350

RESULT 12
 AAB02835
 ID AAB02835 standard; Protein: 350 AA.

XX AAB02835;

DT 22-AUG-2000 (first entry)

XX Human G protein coupled receptor hpprl protein seq ID NO:24.

XX Human; G protein coupled receptor: GPCR; transmembrane receptor;

KW Identification; agonist; screening; therapeutic; pharmaceutical;

XX mutant.

OS Homo sapiens.

XX WO200022131-A2.

XX 20-APR-2000.

XX 13-OCT-1999; 99WO-US24065.

XX 13-OCT-1998; 98US-01170496.

XX 12-NOV-1998; 98US-0108029.

XX 20-NOV-1998; 98US-0109213.

XX 27-NOV-1998; 98US-0110060.

XX 16-FEB-1999; 99US-0120416.

XX 26-FEB-1999; 99US-0121852.

XX 12-MAR-1999; 99US-0123944.

XX 12-MAR-1999; 99US-0123945.

XX 12-MAR-1999; 99US-0123946.

XX 12-MAR-1999; 99US-0123948.

XX 12-MAR-1999; 99US-0123949.

XX 12-MAR-1999; 99US-0123951.

XX 28-MAY-1999; 99US-0136436.

XX 28-MAY-1999; 99US-0136437.

XX 28-MAY-1999; 99US-0136439.

XX 28-MAY-1999; 99US-0137127.

XX 28-MAY-1999; 99US-0137131.

XX 30-JUN-1999; 99US-0141448.

XX 27-AUG-1999; 99US-0151114.

XX 03-SEP-1999; 99US-0152524.

XX 29-SEP-1999; 99US-0156633.

XX 29-SEP-1999; 99US-0156655.

XX 29-SEP-1999; 99US-0156634.

XX (AREN-) ARENA PHARM INC.

PI Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;
 PI Gore M, Liao CW, Lin I, Lowitz K, White C;

DR WPI; 2000-317986/27.

DR N-PSDB; AAA46029.

PT Non-endogenous, human G protein-coupled receptors for screening
 receptor, inverse or partial agonists useful as therapeutic agents

PS Example 1; Page 99-100; 187pp; English.

CC The present invention describes transmembrane receptors, preferably
 CC human G protein coupled receptors (GPCR), for which the endogenous
 CC ligand is unknown (orphan GPCR receptors). More specifically the present
 CC invention relates to non-endogenous, constitutively activated versions
 CC of a human GPCR. These non-endogenous human GPCRs can be useful for

CC the direct identification of candidate compounds as receptors agonists,
 CC inverse agonists or partial agonists for use as pharmaceutical agents.
 CC AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
 CC the exemplification of the present invention.

XX Sequence 350 AA;

Query Match 99.5%; Score 1810; DB 21; Length 350;
 Best Local Similarity 99.4%; Pred. No. 2e-194;
 Matches 348; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MALEONOSTDYEEENMGTYDYSQYELICIKEDVREFAKFLPVLITVIVIGLAGNS 60
 DB 1 MALEONOSTDYEEENMGTYDYSQYELICIKEDVREFAKFLPVLITVIVIGLAGNS 60
 QY 61 MVAIAYAYKKQRTKTDVYILNLAVADLLFLTPFMAVANAHHGWLGKIMKITSALT 120
 DB 61 MVAIAYAYKKQRTKTDVYILNLAVADLLFLTPFMAVANAHHGWLGKIMKITSALT 120
 QY 121 LNFVSGMQLACISIDRYAVATKVPSSGKPCWIIICFCVMAAILLSIPOLVFTYVND 180
 DB 121 LNFVSGMQLACISIDRYAVATKVPSSGKPCWIIICFCVMAAILLSIPOLVFTYVND 180
 QY 181 NARCIPIFRYLGTSKALIQMLEICIGFVVPFLIMGVCFITARTLMKMPNKRISPLK 240
 DB 181 NARCIPIFRYLGTSKALIQMLEICIGFVVPFLIMGVCFITARTLMKMPNKRISPLK 240
 QY 241 VLTFTVIVFTYDLPYNIKFCRAIDIIYSLTSCNMSKRMIDIAIQTESIATLFSCLNP 300
 DB 241 VLTFTVIVFTYDLPYNIKFCRAIDIIYSLTSCNMSKRMIDIAIQTESIATLFSCLNP 300
 QY 301 ILVFMGASFKNYVMKAKKYGSMRROSVSEFPDSEGPTEPTSTFSI 350
 DB 301 ILVFMGASFKNYVMKAKKYGSMRROSVSEFPDSEGPTEPTSTFSI 350

RESULT 13

AAB37788 standard; Protein: 350 AA.

AC AAB37788;

DT 23-FEB-2001 (first entry)

DE Human TSC7.

XX Human: TSC; tuberous sclerosis complex; cytosstatic; antimicrobial;
 KW osteopathic; antitumor; antistimulant; antiallergic; neuroprotective;
 KW cardiant; hypotensive; hypertensive; nootropic; anticonvulsant;
 KW analgesic; tranquilizer; immunosuppressive; anti-inflammatory;
 KW gene therapy; TSC7; infection; cancer; autoimmune disorder;
 KW Parkinson's disease; osteoporosis; neurological disorder.

OS Homo sapiens.

PN WO200064941-A2.

PD 02-NOV-2000.

PE 21-APR-2000; 2000MO-US10979.

PR 23-APR-1999; 9905-0130817.

PR 20-APR-2000; 2000US-0556002.

PA (CURA-) CURAGEN CORP.

PI Gould-Rothberg BE;

WPI; 2000-679670/66.

DR N-PSDB; AAC68722.

PT Novel nucleic acid encoding G-protein coupled receptor for diagnosis
 and treatment of conditions associated with disorder in a G-protein

PT mediated pathway such as cancer, neurological disorders and infections
 PS Claim 12; Page 8; 132pp; English.

XX The present sequence is human tuberous sclerosis complex 7 (TSC7).
 CC TSC7 polynucleotides and polypeptides are useful for determining the
 CC presence or predisposition to a disease associated with altered levels of
 CC TSC7. TSC7 polynucleotides, polypeptides and antibodies specific for the
 CC polypeptide are useful for treating or preventing pathological conditions
 CC associated with the disorder in a G-protein mediated pathway. They are
 CC useful for diagnosing a hyperproliferative condition such as a neoplasm
 CC or dermatological condition. TSC7 nucleic acids and polypeptides are
 CC useful in the treatment of microbial infections, pain, cancer, anorexia,
 CC asthma, autoimmune disorders, Parkinson's disease, acute heart failure,
 CC hypo/hypertension, osteoporosis, multiple sclerosis, angina pectoris,
 CC myocardial infarction, ulcers, allergies, benign prostatic hypertrophy
 CC and psychotic and neurological disorders, including schizophrenia,
 CC dementia, severe mental retardation and dyskinesias, such as
 CC Huntington's disease and/or other pathologies and disorders. TSC7
 CC polypeptides are also useful as immunogens to produce antibodies and as
 CC vaccines.

SQ Sequence 350 AA;

Query Match 99.4%; Score 1808; DB 21; Length 350;
 Best Local Similarity 99.4%; Pred. No. 3.3e-194;
 Matches 348; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALEONOSTDYEEENMGTYDYSQYELICIKEDVREFAKFLPVLITVIVIGLAGNS 60
 DB 1 MALEONOSTDYEEENMGTYDYSQYELICIKEDVREFAKFLPVLITVIVIGLAGNS 60
 QY 61 MVAIAYAYKKQRTKTDVYILNLAVADLLFLTPFMAVANAHHGWLGKIMKITSALT 120
 DB 61 MVAIAYAYKKQRTKTDVYILNLAVADLLFLTPFMAVANAHHGWLGKIMKITSALT 120
 QY 121 LNFVSGMQLACISIDRYAVATKVPSSGKPCWIIICFCVMAAILLSIPOLVFTYVND 180
 DB 121 LNFVSGMQLACISIDRYAVATKVPSSGKPCWIIICFCVMAAILLSIPOLVFTYVND 180
 QY 181 NARCIPIFRYLGTSKALIQMLEICIGFVVPFLIMGVCFITARTLMKMPNKRISPLK 240
 DB 181 NARCIPIFRYLGTSKALIQMLEICIGFVVPFLIMGVCFITARTLMKMPNKRISPLK 240
 QY 241 VLTFTVIVFTYDLPYNIKFCRAIDIIYSLTSCNMSKRMIDIAIQTESIATLFSCLNP 300
 DB 241 VLTFTVIVFTYDLPYNIKFCRAIDIIYSLTSCNMSKRMIDIAIQTESIATLFSCLNP 300
 QY 301 ILVFMGASFKNYVMKAKKYGSMRROSVSEFPDSEGPTEPTSTFSI 350
 DB 301 ILVFMGASFKNYVMKAKKYGSMRROSVSEFPDSEGPTEPTSTFSI 350

RESULT 14

AAY57289 standard; Protein: 333 AA.

AC AAY57289;

DT 05-JUN-2000 (first entry)

DE Human BGCR partial amino acid sequence.

XX BGCR protein: G-protein coupled receptor; human; chemokine; exocytosis;
 KW cell proliferation; anti-inflammatory; anti-angiogenic; antitumor; HIV;
 KW anti-allergic; antiviral.

OS Homo sapiens.

PN WO9952945-A2.

PD 21-OCT-1999.

XX 16-APR-1999; 99MO-US08395.
 XX 16-APR-1998; 98US-0061753.
 PR 16-APR-1999; 99US-0061753.
 XX (MIL-) MILLENITUM PHARM INC.
 XX
 PI Gonzalez JA, Gutierrez-Ramos JC;
 XX
 DR MPI: 1999-620375/53.
 DR N-PSDB: AAZ90527.
 XX
 PT New nucleic acid encoding human BGCKr receptor, used e.g. for
 PT modulating inflammation and tumor growth
 XX
 PS Claim 1; Fig 1A-B; 123pp; English.
 XX
 CC The invention relates to a human BGCKr protein, a G-protein coupled
 CC receptor. The BGCKr protein can be expressed by standard recombinant
 CC methodology. BGCKr are receptor proteins possibly involved in modulation
 CC of proinflammatory or stimulatory functions of chemokines; cell
 CC proliferation, migration, adhesion and targeting, and exocytosis. The
 CC BGCKr nucleic acids and derived proteins (or their variants), antibodies
 CC and modulators are potentially useful for modulating inflammation;
 CC chemotactant activity of leucocytes; angiogenesis; cell proliferation;
 CC tumour growth; allergic reactions and entry of human immune deficiency
 CC virus into cells, for therapeutic or prophylactic purposes. They are also
 CC used for diagnosis and in drug-screening assays. The present sequence
 CC represents the sequence of a partial human BGCKr protein.
 XX
 SQ Sequence 333 AA;

Query Match 95.0%; Score 1728; DB 20; Length 333;
 Best local Similarity 100.0%; Pred. No. 3e-185;
 Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 MNGTYDSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMVAIVAYKKQRTKD 77
 DB 1 MNGTYDSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNSMVAIVAYKKQRTKD 60
 QY 78 VYIINLAVADLLFTLPFMAVNAVHGVNLGKIMCKITSAIYTNFSGMOFLACISIDR 137
 DB 61 VYIINLAVADLLFTLPFMAVNAVHGVNLGKIMCKITSAIYTNFSGMOFLACISIDR 120
 QY 138 YVAATKVPSSQSGVGRPCWIIICFCVMAAIIISIPQLVFYTVNDNARCIPFPRLTGSMT 197
 DB 121 YVAATKVPSSQSGVGRPCWIIICFCVMAAIIISIPQLVFYTVNDNARCIPFPRLTGSMT 180
 QY 198 ALIOMLEICIGFVVPFLIMGVCFITARTLMKMPNIRKISRPKVLTVIVFVITQLPYN 257
 DB 181 ALIOMLEICIGFVVPFLIMGVCFITARTLMKMPNIRKISRPKVLTVIVFVITQLPYN 240
 QY 258 IVKCRADITIIYSLITSCNMSKMDIAIOVTESTALFHSCINPLIYVFMGASFPKNYMKV 317
 DB 241 IVKCRADITIIYSLITSCNMSKMDIAIOVTESTALFHSCINPLIYVFMGASFPKNYMKV 300
 QY 318 AKKYGSMRQROSVSEFPDESGPTSTFSI 350
 DB 301 AKKYGSMRQROSVSEFPDESGPTSTFSI 333

RESULT 15
 AAG67238
 ID AAG67238 standard; Protein: 350 AA.
 XX
 AC AAG67238;
 XX
 DT 13-NOV-2001 (first entry)
 XX
 DE Amino acid sequence of bovine chemokine receptor CCR1.
 XX
 KW Human; chemokine receptor; CCR1; G protein coupled receptor;

KW inflammatory disease; rheumatoid arthritis; inflammatory bowel disease;
 KW asthma; angiogenesis; atherosclerosis vascular association disease;
 KW hypertension; angina pectoris; cardiac arrhythmia; Raynaud's phenomenon;
 KW left ventricular diastolic dysfunction; migraine; preterm labour;
 KW oesophageal spasm; ischemic stroke; subarachnoid haemorrhage;
 KW myocardial infarction; congestive heart failure; endometritis;
 KW vasospasm; retinopathy; nephropathy; pulmonary vascular disease.
 XX
 OS Bos sp.
 XX
 PN WO200166598-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 05-MAR-2001; 2001WO-US07073.
 XX
 PR 03-MAR-2000; 2000US-0186928.
 PR 03-MAR-2000; 2000US-0187231.
 XX
 PA (ICOS-) ICOS CORP.
 XX
 PI Gray PW, Schweickart VL, Epp A, Raport CJ, Chantry D, Steiner B;
 DR MPI: 2001-541918/60.
 DR N-PSDB: AAH77712.

XX
 PS Example 1; Page 99-100; 110pp; English.
 XX
 CC The present sequence represents the bovine chemokine receptor CCR1.
 CC CCR1 is a member of the G protein coupled receptor family. A CCR1
 CC polypeptide, its inhibitor, an antibody, or other modulator of CCR1
 CC expression or biological activity, is useful for treating many
 CC inflammatory diseases, for example, rheumatoid arthritis, inflammatory
 CC bowel disease, and asthma. They are also useful for treating
 CC angiogenesis, atherosclerosis vascular association diseases which may
 CC include but are not limited to hypertension, angina pectoris, cardiac
 CC arrhythmias, left ventricular diastolic dysfunction, Raynaud's
 CC phenomenon, migraine, preterm labour, oesophageal spasm, ischemic
 CC stroke, subarachnoid haemorrhage, myocardial infarction, congestive
 CC heart failure, endometritis, vasospasm, retinopathy, nephropathy, or
 CC pulmonary vascular disease.
 XX
 SQ Sequence 350 AA;

Query Match 89.1%; Score 1620; DB 22; Length 350;
 Best local Similarity 86.0%; Pred. No. 4.2e-173;
 Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

QY 1 MALEONQSDIYYEENMGTYDSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS 60
 DB 1 MALEVQSDIYYEENMGTYDSQYELICIKEDVREFAKVFLPVFLTIVFVIGLAGNS 60
 QY 61 MVAIVAYKKQRTKTDVYIINLAVADLLFTLPFMAVNAVHGVNLGKIMCKITSAIYT 120
 DB 61 TVVAIYAYKKRRTKTDVYIINLAVADLLFTLPFMAVNAVHGVNLGKIMCKITSAIYT 120
 QY 121 LNEVSGMOFLACISIDRYVAATKVPSSQSGVGRPCWIIICFCVMAAIIISIPQLVFYTVND 180
 DB 121 VNEVSGMOFLACISIDRYVAATKVPSSQSGVGRPCWIIICFCVMAAIIISIPQLVFYTVNH 180
 QY 181 NARCIPFPRLTGSMTALIOMLEICIGFVVPFLIMGVCFITARTLMKMPNIRKISRPK 240
 DB 181 KARCVPFPRLTGSMTAKASIQILEICIGFVVPFLIMGVCFITARTLMKMPNIRKISRPK 240
 QY 241 VLTVVIVFVITQLPYNIVKFCRAIDIIYSLITSCNMSKMDIAIOVTESTALFHSCINP 300
 DB 241 VLTVVIVFVITQLPYNIVKFCRAIDIIYSLITSCNMSKMDIAIOVTESTALFHSCINP 300

OY 301 ILYVPMGASFKNYVMKVAKKYGSWMROROSVEEPPDSEGPTEPTSTFSI 350
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
DB 301 VLYVPMGTSPFNKNTMKVAKKYGSMRORONVEIPESEDATEPTSTFSI 350

Search completed: March 14, 2003, 16:11:25
Job time : 38 secs

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 16:09:57 ; Search time 15 seconds
(without alignments)
686.535 Million cell updates/sec

Title: US-09-686-020A-2
Perfect score: 1819
Sequence: 1 MALEQNGSTDYVEENEMNG.....VEEFPDSDGPTPTSTFST 350

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|-------------------|-------------------|
| 1 | 1819 | 100.0 | 350 | 2 | US-08-966-316-16 | Sequence 16, Appl |
| 2 | 1620 | 89.1 | 350 | 2 | US-08-966-316-18 | Sequence 18, Appl |
| 3 | 659 | 36.2 | 358 | 1 | US-08-153-848-19 | Sequence 19, Appl |
| 4 | 659 | 36.2 | 358 | 3 | US-09-299-843A-19 | Sequence 19, Appl |
| 5 | 659 | 36.2 | 358 | 4 | US-09-088-337B-19 | Sequence 19, Appl |
| 6 | 659 | 36.2 | 358 | 5 | PCT-US93-11153-19 | Sequence 19, Appl |
| 7 | 659 | 36.2 | 378 | 1 | US-08-153-848-15 | Sequence 15, Appl |
| 8 | 659 | 36.2 | 378 | 3 | US-09-299-843A-15 | Sequence 15, Appl |
| 9 | 659 | 36.2 | 378 | 4 | US-09-251-545-1 | Sequence 1, Appl |
| 10 | 659 | 36.2 | 378 | 4 | US-09-088-337B-15 | Sequence 15, Appl |
| 11 | 659 | 36.2 | 378 | 5 | PCT-US93-11153-15 | Sequence 15, Appl |
| 12 | 659 | 36.2 | 410 | 1 | US-08-153-848-7 | Sequence 7, Appl |
| 13 | 659 | 36.2 | 410 | 3 | US-09-299-843A-7 | Sequence 7, Appl |
| 14 | 659 | 36.2 | 410 | 4 | US-09-088-337B-7 | Sequence 7, Appl |
| 15 | 659 | 36.2 | 410 | 5 | PCT-US93-11153-7 | Sequence 7, Appl |
| 16 | 650 | 35.7 | 378 | 3 | US-09-299-843A-66 | Sequence 66, Appl |
| 17 | 650 | 35.7 | 378 | 4 | US-09-088-337B-66 | Sequence 66, Appl |
| 18 | 643 | 35.3 | 378 | 1 | US-08-383-750-2 | Sequence 2, Appl |
| 19 | 643 | 35.3 | 378 | 1 | US-08-383-751A-2 | Sequence 2, Appl |
| 20 | 643 | 35.3 | 378 | 3 | US-08-352-678-2 | Sequence 2, Appl |
| 21 | 643 | 35.3 | 378 | 4 | US-09-045-583-49 | Sequence 49, Appl |
| 22 | 643 | 35.3 | 378 | 4 | US-09-534-185-49 | Sequence 49, Appl |
| 23 | 643 | 35.3 | 378 | 5 | PCT-US93-09636-2 | Sequence 2, Appl |
| 24 | 637 | 35.0 | 357 | 4 | US-09-266-464-2 | Sequence 2, Appl |
| 25 | 635.5 | 34.9 | 359 | 1 | US-08-153-848-24 | Sequence 24, Appl |
| 26 | 635.5 | 34.9 | 359 | 3 | US-09-299-843A-24 | Sequence 24, Appl |
| 27 | 635.5 | 34.9 | 359 | 4 | US-09-088-337B-24 | Sequence 24, Appl |

| | | | | | | |
|----|-------|------|-----|---|-------------------|-------------------|
| 28 | 635.5 | 34.9 | 359 | 5 | PCT-US93-11153-24 | Sequence 24, Appl |
| 29 | 606.5 | 33.3 | 361 | 2 | US-08-902-294-2 | Sequence 2, Appl |
| 30 | 606.5 | 33.3 | 361 | 3 | US-09-178-637-2 | Sequence 2, Appl |
| 31 | 583 | 32.1 | 374 | 4 | US-09-045-583-48 | Sequence 48, Appl |
| 32 | 583 | 32.1 | 374 | 4 | US-09-534-185-48 | Sequence 48, Appl |
| 33 | 581 | 31.9 | 342 | 4 | US-09-116-498-4 | Sequence 4, Appl |
| 34 | 569 | 31.3 | 342 | 4 | US-09-116-498-6 | Sequence 6, Appl |
| 35 | 560 | 30.8 | 342 | 2 | US-08-742-011-2 | Sequence 2, Appl |
| 36 | 560 | 30.8 | 342 | 4 | US-09-275-384B-5 | Sequence 5, Appl |
| 37 | 560 | 30.8 | 342 | 4 | US-09-116-498-2 | Sequence 2, Appl |
| 38 | 560 | 30.8 | 342 | 4 | US-09-449-437A-2 | Sequence 2, Appl |
| 39 | 560 | 30.8 | 342 | 4 | US-09-517-605-9 | Sequence 9, Appl |
| 40 | 537.5 | 29.5 | 360 | 4 | US-08-875-573-20 | Sequence 20, Appl |
| 41 | 537.5 | 29.5 | 360 | 4 | US-09-232-878-2 | Sequence 2, Appl |
| 42 | 537.5 | 29.5 | 360 | 4 | US-09-045-583-55 | Sequence 55, Appl |
| 43 | 537.5 | 29.5 | 360 | 4 | US-09-534-185-55 | Sequence 55, Appl |
| 44 | 534.5 | 29.4 | 355 | 1 | US-07-759-568-1 | Sequence 1, Appl |
| 45 | 534.5 | 29.4 | 355 | 1 | US-08-450-393A-8 | Sequence 8, Appl |

ALIGNMENTS

RESULT 1
US-08-966-316-16
Sequence 16, Application US/08966316
Patent No. 593245
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Au-Young, Janice
APPLICANT: Reddy, Roopa
APPLICANT: Murthy, Lynn E.
APPLICANT: Mathur, Preetee
TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/966,316
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0424 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: UTRSNCT11
CLONE: 2547002
US-08-966-316-16

Query Match 100.0%; Score 1819; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.7e-147;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEONOSTDYEEENENNGYDYSQYELICIKEDVREFAKVPFLVETLTVFVIGLAGNS 60
DB 1 MALEONOSTDYEEENENNGYDYSQYELICIKEDVREFAKVPFLVETLTVFVIGLAGNS 60
QY 61 MVAATAYAYKKORFTDYIILNLAVALDLFTLPMAVAVNAHGVWLGIMCKITSALYT 120
DB 61 MVAATAYAYKKORFTDYIILNLAVALDLFTLPMAVAVNAHGVWLGIMCKITSALYT 120
QY 121 LNFVSGMOFLACISIDRYAVATKVPQSOGVKPCWIIICFCVMAAIIILSIPOLVETVND 180
DB 121 LNFVSGMOFLACISIDRYAVATKVPQSOGVKPCWIIICFCVMAAIIILSIPOLVETVND 180
QY 181 NARCIPIPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMPNPKISRLK 240
DB 181 NARCIPIPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMPNPKISRLK 240
QY 241 VLTFTVIVFIVTOLPYNIVKFCRAIDIIYSLITSCNMSKRDIAIOVETISALFHSCLNP 300
DB 241 VLTFTVIVFIVTOLPYNIVKFCRAIDIIYSLITSCNMSKRDIAIOVETISALFHSCLNP 300
QY 301 ILVFMGASFKNYVMKAKKYSWRROQSVVEEPPDSEGTPTSTFSI 350
DB 301 ILVFMGASFKNYVMKAKKYSWRROQSVVEEPPDSEGTPTSTFSI 350

RESULT 2

US-08-966-316-18
Sequence 18, Application US/08966316
Patent No. 5932445

GENERAL INFORMATION:

APPLICANT: Lal, Preeti
APPLICANT: Au-Young, Janice
APPLICANT: Reddy, Roopa E.
APPLICANT: Murthy, Lynn E.
APPLICANT: Mathur, Preete
TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/966,316
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0424 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 399711
US-08-966-316-18

Query Match 89.1%; Score 1620; DB 2; Length 350;
Best Local Similarity 86.0%; Pred. No. 1.4e-130;
Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

QY 1 MALEONOSTDYEEENENNGYDYSQYELICIKEDVREFAKVPFLVETLTVFVIGLAGNS 60
DB 1 MALEONOSTDYEEENENNGYDYSQYELICIKEDVREFAKVPFLVETLTVFVIGLAGNS 60
QY 61 MVAATAYAYKKORFTDYIILNLAVALDLFTLPMAVAVNAHGVWLGIMCKITSALYT 120
DB 61 MVAATAYAYKKORFTDYIILNLAVALDLFTLPMAVAVNAHGVWLGIMCKITSALYT 120
QY 121 LNFVSGMOFLACISIDRYAVATKVPQSOGVKPCWIIICFCVMAAIIILSIPOLVETVND 180
DB 121 LNFVSGMOFLACISIDRYAVATKVPQSOGVKPCWIIICFCVMAAIIILSIPOLVETVND 180
QY 181 NARCIPIPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMPNPKISRLK 240
DB 181 NARCIPIPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMPNPKISRLK 240
QY 241 VLTFTVIVFIVTOLPYNIVKFCRAIDIIYSLITSCNMSKRDIAIOVETISALFHSCLNP 300
DB 241 VLTFTVIVFIVTOLPYNIVKFCRAIDIIYSLITSCNMSKRDIAIOVETISALFHSCLNP 300
QY 301 ILVFMGASFKNYVMKAKKYSWRROQSVVEEPPDSEGTPTSTFSI 350
DB 301 ILVFMGASFKNYVMKAKKYSWRROQSVVEEPPDSEGTPTSTFSI 350

RESULT 3

US-08-153-848-19
Sequence 19, Application US/08153848
Patent No. 5759804

GENERAL INFORMATION:

APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schwellkart, Vicki L.
TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-153-848-19

Query Match 36.2%; Score 659; DB 1: Length 358;
Best Local Similarity 38.7%; Pred. No. 9.7e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

1 MALEONOSTDYEEENMGTYDYSOYELICEDVREFAKVLPVFLTVFVIGLAGNS 60
1 VCLQDEVDYIDGNT---TVDTLFEISCKSKDVNFKAMFLPIVMSIICFVGLGNG 57
61 MVAIYAYVKKORTKTDVYILNLAVADLLFTLPFAVNAVHGVGLKIMCKITSAIYT 120
58 LVVLYIYFKRKTMDTYLLNLAVADILFTLPFAVNAVHGVGLKIMCKITSAIYT 117
121 LNFVSGMQLACISIDRYAVATKVP---QSGVGKPCWICFCVMAAILSLIPOLVY 176
118 MSFSGMQLLCISIDRYAVATKVP---QSGVGKPCWICFCVMAAILSLIPOLVY 177
177 TVNDNA-----RCIPFPRLGTSMKALIQMLEICIGFVPLMGVCYFTARTLMKP 231
178 DLQSSSEQAMRCSLITEH---VEAFITIQVAVMIGFLVPLAMSFVYVITRLLOAR 234
232 NIKISRLKVLTVVIVFVITOLPYNIYKFCRAIDIIYSLTSCNMSKRMDAIOVTEFI 291
235 NFEHNKAIKVIAVVFVIFOLPYNGVLAQTVANFNITSTCLSKQNLINADVTYSL 294
292 ALFHSCLNPLIYVFMGASFKNYVAKKYG-----SW-----RRORSVEEPPD 337
295 ACVRCVNPFLIYAFVIGKRNDFKLFKDLGCLSQDLRQMSCHIRSSMSVE----- 349
338 SEGPTPEPTSPFS 349
350 ---AETTTTFS 357

RESULT 4
US-09-299-843A-19
Sequence 19, Application US/09299843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schwellkart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848

FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-843A-19

Query Match 36.2%; Score 659; DB 3: Length 358;
Best Local Similarity 38.7%; Pred. No. 9.7e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

1 MALEONOSTDYEEENMGTYDYSOYELICEDVREFAKVLPVFLTVFVIGLAGNS 60
1 VCLQDEVDYIDGNT---TVDTLFEISCKSKDVNFKAMFLPIVMSIICFVGLGNG 57
61 MVAIYAYVKKORTKTDVYILNLAVADLLFTLPFAVNAVHGVGLKIMCKITSAIYT 120
58 LVVLYIYFKRKTMDTYLLNLAVADILFTLPFAVNAVHGVGLKIMCKITSAIYT 117
121 LNFVSGMQLACISIDRYAVATKVP---QSGVGKPCWICFCVMAAILSLIPOLVY 176
118 MSFSGMQLLCISIDRYAVATKVP---QSGVGKPCWICFCVMAAILSLIPOLVY 177
177 TVNDNA-----RCIPFPRLGTSMKALIQMLEICIGFVPLMGVCYFTARTLMKP 231
178 DLQSSSEQAMRCSLITEH---VEAFITIQVAVMIGFLVPLAMSFVYVITRLLOAR 234
232 NIKISRLKVLTVVIVFVITOLPYNIYKFCRAIDIIYSLTSCNMSKRMDAIOVTEFI 291
235 NFEHNKAIKVIAVVFVIFOLPYNGVLAQTVANFNITSTCLSKQNLINADVTYSL 294
292 ALFHSCLNPLIYVFMGASFKNYVAKKYG-----SW-----RRORSVEEPPD 337
295 ACVRCVNPFLIYAFVIGKRNDFKLFKDLGCLSQDLRQMSCHIRSSMSVE----- 349
338 SEGPTPEPTSPFS 349
350 ---AETTTTFS 357

RESULT 5
US-09-088-337B-19
Sequence 19, Application US/09088337B
Patent No. 6348574
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schwellkart, Vicki L.
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

```

;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/088,337B
; FILING DATE: 01-Jun-1998
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6348574and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
;
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-088-337B-19

Query Match 36.2%; Score 659; DB 4; Length 358;
Best Local Similarity 38.7%; Pred. No. 9.7e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MALEBONSTDIYYENENGTYYDSOYELICIKEDVREFAKVPFLPVLITVIVGLAGNS 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   1 VCLCODEVTDDYIGDNT--TVDYTLFESLCSKRDVRNFKAMFLPIMYSIICFVGLGNG 57
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 MVAALIVAYKKQKRTQVYIINLAVADLLFLTPFMAVNAVHGVGLCKIMCKITSALYT 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   58 LVVLTYIYFKRLKMTDTYLLNLAVADLLFLTPFMAVSAKSMVGVHCKKLIYALYK 117
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 121 LNFVSGMOFLACISIDRVATKVP-----OSGVKPCMIICFCVMAAAILLSIPOLVEY 176
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   118 MSFSGMILLICISIDRVAVAVQAVSAHRHARVLLSKLSCVGIWILATVLSPELLYS 177
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 177 TVNDNA-----RCIPFPRYLGTSMAKLIOMLEICIGFVVPFLIMGYCYFTARTLKM 231
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   178 DLQSSSEQAMRCSLITEH--VEAFITIQVAVQVIGFVPLLMSCYLIYIRTLQAR 234
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 232 NIKISRLKVLIVYIYQLPYNIYKFCRAIDIIYSLTSCNMSKRMADIAQVTEST 291
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   235 NFERNKAIKVIIVAVVFIYQLPYNGVLAQTVANFNITSTCELSQOLMIAVDVYSL 294
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 292 ALPHSCLPILYVPMGASFKNYKVAKKYG-----SW-----PRQOSVEEPPED 337
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   295 ACVRCVCYNPFLIAYIGKFRNDLFKLRDGLCSQEQOLRQMSCHRIHRRSMASVE----- 349
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 338 SEGTEPTSTFS 349
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   350 ----AETTTTFS 357
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
PCT-US93-11153-19
; Sequence 19, Application PC/TUS9311153
; GENERAL INFORMATION:
; APPLICANT: Godtska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schmeikart, Vicki L.
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
```

```

; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11153
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
;
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US93-11153-19

Query Match 36.2%; Score 659; DB 5; Length 358;
Best Local Similarity 38.7%; Pred. No. 9.7e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MALEBONSTDIYYENENGTYYDSOYELICIKEDVREFAKVPFLPVLITVIVGLAGNS 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   1 VCLCODEVTDDYIGDNT--TVDYTLFESLCSKRDVRNFKAMFLPIMYSIICFVGLGNG 57
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 MVAALIVAYKKQKRTQVYIINLAVADLLFLTPFMAVNAVHGVGLCKIMCKITSALYT 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   58 LVVLTYIYFKRLKMTDTYLLNLAVADLLFLTPFMAVSAKSMVGVHCKKLIYALYK 117
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 121 LNFVSGMOFLACISIDRVATKVP-----OSGVKPCMIICFCVMAAAILLSIPOLVEY 176
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   118 MSFSGMILLICISIDRVAVAVQAVSAHRHARVLLSKLSCVGIWILATVLSPELLYS 177
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 177 TVNDNA-----RCIPFPRYLGTSMAKLIOMLEICIGFVVPFLIMGYCYFTARTLKM 231
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   178 DLQSSSEQAMRCSLITEH--VEAFITIQVAVQVIGFVPLLMSCYLIYIRTLQAR 234
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 232 NIKISRLKVLIVYIYQLPYNIYKFCRAIDIIYSLTSCNMSKRMADIAQVTEST 291
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   235 NFERNKAIKVIIVAVVFIYQLPYNGVLAQTVANFNITSTCELSQOLMIAVDVYSL 294
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 292 ALPHSCLPILYVPMGASFKNYKVAKKYG-----SW-----PRQOSVEEPPED 337
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   295 ACVRCVCYNPFLIAYIGKFRNDLFKLRDGLCSQEQOLRQMSCHRIHRRSMASVE----- 349
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 338 SEGTEPTSTFS 349
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
   350 ----AETTTTFS 357
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
US-08-153-848-15
; Sequence 15, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godtska, Ronald
```

APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-153-848-15

Query Match 36.2%; Score 659; DB 1; Length 378;
Best Local Similarity 38.7%; Pred. No. 1e-48;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;
QY 1 MALEONOSTDYEEENEMNGTYDSQYELICIKEDVREFAVPFLPVFLTIVFVIGLAGNS 60
DB 21 VCLCODEVTDDYIGDNT---IVDTLTFESLCSKDVNRNFKAMFLPIMYSITICFVGLGNG 77
QY 61 MVAATYAYVYKQRTKTDVYIINLAVADLLFLTPFMAVNAHGVGLGKIMCKITSAIYT 120
DB 78 LVLLTYIFKRLKMTDYLNLAVADLLFLTPFMAVSAKSWFVGHFCKLIFAIYK 137
QY 121 LNFVSGMPLACISIDRYVAATKVP---QSGVGRPCWITICFVMAAIIISIPOLVFY 176
DB 138 MSFSGMALLCISIDRYVAIVQAVSAHRRARVLLISKSCVGIWILATVLSIPELLYS 197
QY 177 TVNDNA-----RCIPFPRYLGTSMKALIQMLEICIGFVFPFLMGVCFYFARTLMKMP 231
DB 198 DLORSSSQAMRCSLITEH---VEAFITIQVAGWIGFVPLLMASFCYIVIRILLQAR 254
QY 233 NIKISRLKVLITVIVIVEITQLPYNIIVKFCRAIDIIYSLTSCMSKRDIAIQVETSI 291
DB 255 NFERKKAIRKIIAIVVVEIVFQLPYNGVLAQTVANFNITSSTCELKQNLIAVDVYSL 314
QY 292 ALPHSCINILIVFMGASFKNYVMVAKKYG-----SW-----RROQSVEEFEPFD 337
DB 315 ACVRCVNFELIYAFIGVAFRNDLFKFLDGLQSOQLRQSSCHRIHRSMSAYE----- 369
QY 338 SEGTEPTSTFS 349
DB 370 ----AETTTTFS 377

RESULT 8
US-09-299-843A-15
Sequence 15, Application US/09299843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-843A-15
Query Match 36.2%; Score 659; DB 3; Length 378;
Best Local Similarity 38.7%; Pred. No. 1e-48;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;
QY 1 MALEONOSTDYEEENEMNGTYDSQYELICIKEDVREFAVPFLPVFLTIVFVIGLAGNS 60
DB 21 VCLCODEVTDDYIGDNT---IVDTLTFESLCSKDVNRNFKAMFLPIMYSITICFVGLGNG 77
QY 61 MVAATYAYVYKQRTKTDVYIINLAVADLLFLTPFMAVNAHGVGLGKIMCKITSAIYT 120
DB 78 LVLLTYIFKRLKMTDYLNLAVADLLFLTPFMAVSAKSWFVGHFCKLIFAIYK 137
QY 121 LNFVSGMPLACISIDRYVAATKVP---QSGVGRPCWITICFVMAAIIISIPOLVFY 176
DB 138 MSFSGMALLCISIDRYVAIVQAVSAHRRARVLLISKSCVGIWILATVLSIPELLYS 197
QY 177 TVNDNA-----RCIPFPRYLGTSMKALIQMLEICIGFVFPFLMGVCFYFARTLMKMP 231
DB 198 DLORSSSQAMRCSLITEH---VEAFITIQVAGWIGFVPLLMASFCYIVIRILLQAR 254
QY 233 NIKISRLKVLITVIVIVEITQLPYNIIVKFCRAIDIIYSLTSCMSKRDIAIQVETSI 291

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Db      255 NFERKAKIVIAVAVVIVFQLPYNGVLAQVAVANENITSTCELSQVLAIVADVYSL 314
QY      292 ALFHSCNLPILYVEMGASFKNYVVKAKKYG-----SW-----RROQSVEEPPD 337
Db      315 ACVRCVNPFLYAFIGVAFKFRNDLFKFLDGLCLOEQVLRQMSCRHTRRSMYSVE----- 369
QY      338 SEGTEPTSTPS 349
Db      370 -----AETTTTFS 377

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RESULT 9

US-09-251-545-1

; Sequence 1, Application US/09251545

; Patent No. 6153441

; GENERAL INFORMATION:

; APPLICANT: Edward R. Appelbaum

; APPLICANT: Henry M. Sarau

; APPLICANT: John R. White

; TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND

; TITLE OF INVENTION: ANTAGONISTS OF THE INTERACTION BETWEEN HUMAN CCR7 RECEPTOR

; FILE REFERENCE: P50753

; CURRENT APPLICATION NUMBER: US/09/251,545

; EARLIER FILING DATE: 1999-02-17

; EARLIER APPLICATION NUMBER: 60/074,883

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO: 1

; LENGTH: 378

; TYPE: PRT

; ORGANISM: Human

US-09-251-545-1

Query Match 36.2%; Score 659; DB 4; Length 378;

Best Local Similarity 38.7%; Pred. No. 1e-48;

Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

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QY      1  MLEBONOSTDYVEENENNGTYDYISOYELICIKEDYREPAKVELPVLITVIVGIGLAGNS 60
Db      21  VCLQDEVTDDYIGDNT---TVDTYLFESLCSKKDVNFKAMFLPIMYSIICFVGLLNG 77
QY      61  MVAIVAYYKQKRTDYIILNLAVALDLLFTLPFMAVNAVHGVLGKIMCKITSALYT 120
Db      78  LVLVLYYFKRLKMTDTYLLNLAVADILFTLPFMAVSAKSWFVGHCKLIFALYK 137
QY      121  LNFVSGMOFLACISIDRYAVATKVP-----OSGVKPCWIIICFCVMAAAILLSIPOLVY 176
Db      138  MSFSSGMLLICISIDRYAVAVQAVSAHRHARVLLISKSCVGIWILATVLSIPELLYS 197
QY      177  TVNDNA-----RCIPIPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMKP 231
Db      198  DLORSSSEQAMRCSLITEH---VEAFITIOVAQWIGFVLPLAMSFYLVITRLLQAR 254
QY      232  NIKISRPLKVLTVIVYFYTOLPYNIVKFCRAIDIIYSLTSCMSKRMADIAIQVTEST 291
Db      255  NFERKAKIVIAVAVVIVFQLPYNGVLAQVAVANENITSTCELSQVLAIVADVYSL 314
QY      292  ALFHSCNLPILYVEMGASFKNYVVKAKKYG-----SW-----RROQSVEEPPD 337
Db      315  ACVRCVNPFLYAFIGVAFKFRNDLFKFLDGLCLOEQVLRQMSCRHTRRSMYSVE----- 369
QY      338  SEGTEPTSTPS 349
Db      370  -----AETTTTFS 377

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RESULT 10

US-09-088-337B-15

; Sequence 15, Application US/09088337B

; Patent No. 6348574

```

; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; Gray, Patrick W.
; Schwellkart, Vicki L.
; TITLE OF INVENTION: No. 6348574e1 Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray &
; Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/088,337B
; FILING DATE: 01-Jun-1998
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6348574and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-088-337B-15

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Query Match 36.2%; Score 659; DB 4; Length 378;

Best Local Similarity 38.7%; Pred. No. 1e-48;

Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

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QY      1  MLEBONOSTDYVEENENNGTYDYISOYELICIKEDYREPAKVELPVLITVIVGIGLAGNS 60
Db      21  VCLQDEVTDDYIGDNT---TVDTYLFESLCSKKDVNFKAMFLPIMYSIICFVGLLNG 77
QY      61  MVAIVAYYKQKRTDYIILNLAVALDLLFTLPFMAVNAVHGVLGKIMCKITSALYT 120
Db      78  LVLVLYYFKRLKMTDTYLLNLAVADILFTLPFMAVSAKSWFVGHCKLIFALYK 137
QY      121  LNFVSGMOFLACISIDRYAVATKVP-----OSGVKPCWIIICFCVMAAAILLSIPOLVY 176
Db      138  MSFSSGMLLICISIDRYAVAVQAVSAHRHARVLLISKSCVGIWILATVLSIPELLYS 197
QY      177  TVNDNA-----RCIPIPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMKP 231
Db      198  DLORSSSEQAMRCSLITEH---VEAFITIOVAQWIGFVLPLAMSFYLVITRLLQAR 254
QY      232  NIKISRPLKVLTVIVYFYTOLPYNIVKFCRAIDIIYSLTSCMSKRMADIAIQVTEST 291
Db      255  NFERKAKIVIAVAVVIVFQLPYNGVLAQVAVANENITSTCELSQVLAIVADVYSL 314
QY      292  ALFHSCNLPILYVEMGASFKNYVVKAKKYG-----SW-----RROQSVEEPPD 337
Db      315  ACVRCVNPFLYAFIGVAFKFRNDLFKFLDGLCLOEQVLRQMSCRHTRRSMYSVE----- 369

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Db 230 DLORSSSEQAMRCSLITEH---VEAFITIOVAMVIGFLVPLLLAMSFICYLVIIRTLLOAR 286
QY 232 NIKISRPLKVLTVIVFIVTOLPYNIYKFCRAIDIIISLITSCNMKRMIDIAIOVTSI 291
Db 287 NERNKAIRKVIIVAVVVFIVFOLPYNGVLAOTVANFNITSSITCBLSKOULNADVYSL 346
QY 292 ALFHSCNPLILVYFMGASFKNVYKAKYK-----SW-----RROKOSVEEFPD 337
Db 347 ACVRCVNPFLVAFIGVKFRNDLFKFDLGLSOLRQMSCHIRRSSMSVE----- 401
QY 338 SEGPTEPTSTFS 349
Db 402 ---AETTTTFS 409
RESULT 13
US-09-299-843A-7
Sequence 7, Application US/09299843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweiart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/320598
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-843A-7
Query Match 36.2%, Score 659, DB 3; Length 410;
Best Local Similarity 38.7%, Pred. No. 1,le-48;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;
QY 1 MALBQNSTDYIYENENANGTYDYSQYELLCIKEDVREFAVPLPVLITVIVIGLAGNS 60

Db 53 VCLQCDVETDIDYDNT---TVDYTLFESLCSKDKVRNFRAMPFLPIMYSIICFVGLLNG 109
QY 61 MVAIVAYIRYKQRTKDYVILNLNAVADLLFLPFRANAVAVGVULGIMKITYALT 120
Db 110 LVVLTITYFRKLTMDTYLLNLAVADILFLPLFRMAVSAAASWEGVHFCFLIPIAYK 169
QY 121 LNFSGQFLACISIDRYVAVTKVPS---QSGVGKRCWITICFVMAAILISIPOLVY 176
Db 170 MSFFSGMLLICSIDRYVAIVAVSAHRRARVLLSKISCGVITLAVLSIPELIS 229
QY 177 TVNDNA-----KCIPIEPRYLGTSMAALIOMLEICIGFVVPFLIMGVCFYIARTLMKP 231
Db 230 DLORSSSEQAMRCSLITEH---VEAFITIOVAMVIGFLVPLLLAMSFICYLVIIRTLLOAR 286
QY 232 NIKISRPLKVLTVIVFIVTOLPYNIYKFCRAIDIIISLITSCNMKRMIDIAIOVTSI 291
Db 287 NERNKAIRKVIIVAVVVFIVFOLPYNGVLAOTVANFNITSSITCBLSKOULNADVYSL 346
QY 292 ALFHSCNPLILVYFMGASFKNVYKAKYK-----SW-----RROKOSVEEFPD 337
Db 347 ACVRCVNPFLVAFIGVKFRNDLFKFDLGLSOLRQMSCHIRRSSMSVE----- 401
QY 338 SEGPTEPTSTFS 349
Db 402 ---AETTTTFS 409

RESULT 14
US-09-088-337B-7
Sequence 7, Application US/09088337B
Patent No. 6348574
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweiart, Vicki L.
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-JUN-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7
US-09-088-337B-7

Query Match 36.2%; Score 659; DB 4; Length 410;
Best Local Similarity 38.7%; Pred. No. 1.1e-48;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MALEONOSTDYEEENMGNGYDSOYELICIKEDVREFAKVFLEPFLTVFVIGLAGNS 60
DB 53 VCLCQDEVTDDYIDGNT---TVDYTLFESLCSKRDVNFAMFLPMISLTCVGLLNG 109
QY 61 MVAIAYYKKORTKTDVYILMLAVADLLFTLPFWAVNAVHGVLGKIMCKITSALYT 120
DB 110 LVLTLYIFKRLKMTDYLMLAVADLLFTLPFWAVNAVHGVLGKIMCKITSALYT 169
QY 121 LNFVSGMFLACISIDRYAVATKVP---OSGVGKPCWIIICFCVMAAILSTPOLVFY 176
DB 170 MSFSGMLLLCISIDRYAVATKVP---OSGVGKPCWIIICFCVMAAILSTPOLVFY 229
QY 177 TVNDNA-----RCIPFPRLTGTSMKALIMLEICIGFVVPFLMGVCYFTRTLMKMP 231
DB 230 DLQSSSEQAMRCSLITEH---VEAFITQVAGVIGFVPLAMSCYIVITRTLLQAR 286
QY 232 NIKISRLKVLVTVIVFVITQLPYNTKFCRAIDITISLITSCNSKRMIDAIOVTEST 291
DB 287 NFERNKAIKVIIVAVVVFVIFQLPYNGVLAQTVANFNITSTCELSKQNLNAVDTYSL 346
QY 292 ALFHSCLNPLIYVFMGASFKNYVMKAKYG-----SW-----RRROSVEEPPD 337
DB 347 ACVRCVNPFLYAFIVGKFRNDLFKLDGCLSGQLRWSSCHIRSSMSVE----- 401
QY 338 SEGTEPTSTFS 349
DB 402 ----AETTTFS 409

RESULT 15
PCT-US93-11153-7
Sequence 7, Application PC/TUS9311153

GENERAL INFORMATION:

APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schmelkart, Vicki L.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452

ATTORNEY/AGENT INFORMATION:

NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448

TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-11153-7

Query Match 36.2%; Score 659; DB 5; Length 410;
Best Local Similarity 38.7%; Pred. No. 1.1e-48;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MALEONOSTDYEEENMGNGYDSOYELICIKEDVREFAKVFLEPFLTVFVIGLAGNS 60
DB 53 VCLCQDEVTDDYIDGNT---TVDYTLFESLCSKRDVNFAMFLPMISLTCVGLLNG 109
QY 61 MVAIAYYKKORTKTDVYILMLAVADLLFTLPFWAVNAVHGVLGKIMCKITSALYT 120
DB 110 LVLTLYIFKRLKMTDYLMLAVADLLFTLPFWAVNAVHGVLGKIMCKITSALYT 169
QY 121 LNFVSGMFLACISIDRYAVATKVP---OSGVGKPCWIIICFCVMAAILSTPOLVFY 176
DB 170 MSFSGMLLLCISIDRYAVATKVP---OSGVGKPCWIIICFCVMAAILSTPOLVFY 229
QY 177 TVNDNA-----RCIPFPRLTGTSMKALIMLEICIGFVVPFLMGVCYFTRTLMKMP 231
DB 230 DLQSSSEQAMRCSLITEH---VEAFITQVAGVIGFVPLAMSCYIVITRTLLQAR 286
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DB 287 NFERNKAIKVIIVAVVVFVIFQLPYNGVLAQTVANFNITSTCELSKQNLNAVDTYSL 346
QY 292 ALFHSCLNPLIYVFMGASFKNYVMKAKYG-----SW-----RRROSVEEPPD 337
DB 347 ACVRCVNPFLYAFIVGKFRNDLFKLDGCLSGQLRWSSCHIRSSMSVE----- 401
QY 338 SEGTEPTSTFS 349
DB 402 ----AETTTFS 409

Search completed: March 14, 2003, 16:12:09
Job time: 17 secs

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 16:12:17 ; Search time 14 Seconds
(without alignments)
1152.302 Million cell updates/sec

Title: US-09-686-020A-2

Perfect score: 1819

Sequence: 1 MALEQNSQSDYYEENEMNG.....VEPPFDSGPTPTSTFSI 350

Scoring table: ELOSUM62

Gapop 10.0 , Gapext 0.5

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications-AA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 1819 | 100.0 | 350 | 10 | US-09-796-338A-8 |
| 3 | 1814 | 99.7 | 349 | 9 | US-09-765-994-4 |
| 4 | 761 | 41.8 | 175 | 9 | US-09-989-442-108 |
| 5 | 761 | 41.8 | 175 | 9 | US-10-073-865-91 |
| 6 | 761 | 41.8 | 175 | 10 | US-09-764-853-584 |
| 7 | 637 | 35.0 | 357 | 9 | US-09-966-755-2 |
| 8 | 637 | 35.0 | 357 | 10 | US-09-903-377-2 |
| 9 | 637 | 35.0 | 357 | 10 | US-09-952-385-2 |
| 10 | 637 | 35.0 | 357 | 12 | US-10-000-759A-2 |
| 11 | 581 | 31.9 | 342 | 10 | US-09-852-156-4 |
| 12 | 569 | 31.3 | 342 | 10 | US-09-852-156-6 |
| 13 | 560 | 30.8 | 342 | 10 | US-09-852-156-2 |
| 14 | 560 | 30.8 | 342 | 10 | US-09-940-063-2 |
| 15 | 537.5 | 29.5 | 360 | 9 | US-10-120-394-20 |
| 16 | 537.5 | 29.5 | 360 | 9 | US-09-764-413-20 |
| 17 | 537.5 | 29.5 | 360 | 10 | US-09-837-446-2 |
| 18 | 537.5 | 29.5 | 360 | 10 | US-09-766-744-17 |
| 19 | 532.5 | 29.3 | 360 | 10 | US-09-938-719-10 |

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| 20 | 532.5 | 29.3 | 360 | 10 | US-09-939-226-10 | Sequence 10, Appl |
| 21 | 532.5 | 29.3 | 360 | 10 | US-09-938-703-10 | Sequence 10, Appl |
| 22 | 526.5 | 28.9 | 362 | 10 | US-09-898-751A-4 | Sequence 4, Appl |
| 23 | 525 | 28.9 | 362 | 10 | US-09-931-381A-18 | Sequence 18, Appl |
| 24 | 522.5 | 28.7 | 355 | 10 | US-09-789-482-4 | Sequence 4, Appl |
| 25 | 522.5 | 28.7 | 355 | 10 | US-09-789-486-4 | Sequence 4, Appl |
| 26 | 518.5 | 28.5 | 362 | 9 | US-09-898-751A-2 | Sequence 2, Appl |
| 27 | 515.5 | 28.3 | 361 | 10 | US-09-931-381A-20 | Sequence 20, Appl |
| 28 | 500.5 | 27.5 | 352 | 10 | US-09-104-063-2 | Sequence 4, Appl |
| 29 | 500.5 | 27.5 | 352 | 10 | US-09-953-692-2 | Sequence 2, Appl |
| 30 | 500.5 | 27.5 | 352 | 10 | US-09-953-717-2 | Sequence 2, Appl |
| 31 | 498.5 | 27.4 | 352 | 9 | US-09-870-759-37 | Sequence 37, Appl |
| 32 | 498.5 | 27.4 | 352 | 9 | US-09-870-759-144 | Sequence 144, App |
| 33 | 497 | 27.3 | 360 | 10 | US-09-938-719-7 | Sequence 7, Appl |
| 34 | 497 | 27.3 | 360 | 10 | US-09-939-226-7 | Sequence 7, Appl |
| 35 | 497 | 27.3 | 360 | 10 | US-09-938-703-7 | Sequence 7, Appl |
| 36 | 492 | 27.0 | 347 | 10 | US-09-104-792-3 | Sequence 3, Appl |
| 37 | 492 | 27.0 | 360 | 10 | US-09-131-827A-2 | Sequence 2, Appl |
| 38 | 491.5 | 27.0 | 352 | 12 | US-10-106-623-20 | Sequence 20, Appl |
| 39 | 491 | 27.0 | 360 | 10 | US-09-131-827A-20 | Sequence 20, Appl |
| 40 | 486.5 | 26.7 | 350 | 9 | US-09-104-063-2 | Sequence 83, Appl |
| 41 | 486.5 | 26.7 | 350 | 10 | US-09-782-980-83 | Sequence 2, Appl |
| 42 | 486.5 | 26.7 | 350 | 10 | US-09-884-430-7 | Sequence 7, Appl |
| 43 | 486 | 26.7 | 355 | 10 | US-09-104-792-2 | Sequence 2, Appl |
| 44 | 484.5 | 26.6 | 352 | 9 | US-10-232-666-2 | Sequence 2, Appl |
| 45 | 484.5 | 26.6 | 352 | 10 | US-09-725-285-2 | Sequence 2, Appl |

ALIGNMENTS

RESULT 1
US-09-765-994-2 Application US/09765994
; Sequence 2, Appl
; Patent No. US20010016336A1
; GENERAL INFORMATION:
; APPLICANT: ELLIS, CATHERINE
; TITLE OF INVENTION: THE G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: GH-70225-C1
; CURRENT APPLICATION NUMBER: US/09/765,994
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/053,895
; PRIOR FILING DATE: 1997-08-15
; PRIOR APPLICATION NUMBER: 08/962,922
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 350
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-765-994-2

Query Match 100.0%, Score 1819, DB 10, Length 350;
Best Local Similarity 100.0%, Pred. No. 5.7e-153; Indels 0;
Matches 350; Conservative 0; Mismatches 0; Gaps 0;

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| QY | 1 | MALEQNSQSDYYEENEMNGTDY | SOYELICIKEDREFAKFLPVLFTIVIGLAGNS | 60 |
| DB | 1 | MALEQNSQSDYYEENEMNGTDY | SOYELICIKEDREFAKFLPVLFTIVIGLAGNS | 60 |
| QY | 61 | MVAIAYKKKQTKDYVTLNADV | LLFLTPMAVNAVHGVNIGKIMKITSALYT | 120 |
| DB | 61 | MVAIAYKKKQTKDYVTLNADV | LLFLTPMAVNAVHGVNIGKIMKITSALYT | 120 |
| QY | 121 | LNFSGMOPLACISIDRYAVTK | VPQSOGVGRKWCITCVMMAATLISIPQVFTVND | 180 |
| DB | 121 | LNFSGMOPLACISIDRYAVTK | VPQSOGVGRKWCITCVMMAATLISIPQVFTVND | 180 |
| QY | 181 | NARCIPLFPYLTGTSKALQML | EICIGFVPLPLINGCYFTARTLMKPNIKISRLK | 240 |
| DB | 181 | NARCIPLFPYLTGTSKALQML | EICIGFVPLPLINGCYFTARTLMKPNIKISRLK | 240 |

| Qy | Dy | Qy | Dy |
|-----|---|-----|---|
| 241 | VLTVNVEIYTOLPYNNVKKRCRAIDIIYSLTSCNNKSRKDIAIQVTEBIALEFHSCLNP | 301 | ILYVFMGASFNNYMKYAKKKGSMRRORQSYEEFPDPSGEGTEPTSTFSI 350 |
| 241 | VLTVNVEIYTOLPYNNVKKRCRAIDIIYSLTSCNNKSRKDIAIQVTEBIALEFHSCLNP | 301 | ILYVFMGASFNNYMKYAKKKGSMRRORQSYEEFPDPSGEGTEPTSTFSI 350 |
| 241 | VLTVNVEIYTOLPYNNVKKRCRAIDIIYSLTSCNNKSRKDIAIQVTEBIALEFHSCLNP | 301 | ILYVFMGASFNNYMKYAKKKGSMRRORQSYEEFPDPSGEGTEPTSTFSI 350 |

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1 RESULT 2
2 US-09-796-338A-8
3 : Sequence 8, Application US/09796338A
4 : Patent No. US20020061522A1
5 : GENERAL INFORMATION:
6 : APPLICANT: Millennium Pharmaceuticals, Inc.
7 : TITLE OF INVENTION: 1983, 52881, 2398, 45449, 50289, AND
8 : TITLE OF INVENTION: 52872, NOVEL G PROTEIN-COUPLED RECEPTORS AND USES THEREFOR
9 : FILE REFERENCE: 10448-020001
10 : CURRENT APPLICATION NUMBER: US/09/796,338A
11 : CURRENT FILING DATE: 2001-02-28
12 : PRIOR APPLICATION NUMBER: 05/60/186,059
13 : PRIOR FILING DATE: 2000-02-29
14 : NUMBER OF SEQ ID NOS: 26
15 : SOFTWARE: FastSeq for Windows Version 4.0
16 : SEQ ID NO 8
17 : LENGTH: 350
18 : TYPE: PRT
19 : ORGANISM: Homo sapiens
20 : US-09-796-338A-8

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| Query Match | 100.0% | Score 1819; | DB 10; | Length 350; |
| Best Local Similarity | 100.0% | Pred. No. 5.7e-153; | | |
| Matches 350; Conservative | 0; | Mismatches | 0; | Indels 0; Gaps 0; |

| | | | |
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| QY | 1 | MALRONOSTDYVEEENENENGGYDYSOXELICIKEDVAEPKVFPLPVLTIVFPIGLAGNS | 60 |
| Db | 1 | MALQONOSTDYVEEENENENGGYDYSQXELICIKEDVAEPKVFPLPVLTIVFPIGLAGNS | 60 |
| QY | 61 | MVAIAVAYKKQRTDVTYILINLAVADLLFTLPENAVANAQWVLGKIMCKITSALYT | 120 |
| Db | 61 | MVAIAVAYKKQRTDVTYILINLAVADLLFTLPENAVANAQWVLGKIMCKITSALYT | 120 |
| QY | 121 | LNFSVGMQFLACISIDRYVAATKVPSOSGVGKPCWIIICFCVMAAILLSIPQLVFTYVND | 180 |
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| QY | 181 | NARCIPFPRYLGTSMKALLOMETICIGEVAVPFLIMGVCFITARTLMPKNIKISBPX | 240 |
| Db | 181 | NARCIPFPRYLGTSMKALLOMETICIGEVAVPFLIMGVCFITARTLMPKNIKISBPX | 240 |
| QY | 241 | VLLTVVIVFITYTOLPYNINIVFCRAIDIIYSILTSNCKNSKRMDAIQVTEISIALFHSCLNP | 300 |
| Db | 241 | VLLTVVIVFITYTOLPYNINIVFCRAIDIIYSILTSNCKNSKRMDAIQVTEISIALFHSCLNP | 300 |
| QY | 301 | ILYVFMGASFKNYMKVAKKXGSRROROSVEEPPPESEPTPTSFESI | 350 |
| Db | 301 | ILYVFMGASFKNYMKVAKKXGSRROROSVEEPPPESEPTPTSFESI | 350 |

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RESULT 3
US-09-765-994-A
: Sequence 4, Application US/09765994
: Patent No. US2001001636A1
: GENERAL INFORMATION:
: APPLICANT: ELLIS, CATHERINE
: TITLE OF INVENTION: THE G-PROTEIN COUPLED RECEPTOR
: TITLE OF INVENTION: (HFTA041)
: FILE REFERENCE: GH-70225-C1
: CURRENT APPLICATION NUMBER: US/09/765,994
: CURRENT FILING DATE: 2001-01-19
: PRIOR APPLICATION NUMBER: 60/055,895
: PRIOR FILING DATE: 1997-08-15

```

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? PRIOR APPLICATION NUMBER: 08/962,922
?
? PRIOR FILING DATE: 1997-10-27
?
? NUMBER OF SEQ ID NOS: 4
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? SOFTWARE: FASTSQ for Windows Version 3.0
?
? SEQ ID NO. 4
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? LENGTH: 349
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? TYPE: PRT
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? ORGANISM: HOMO SAPIENS
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? OS-09-765-994-4

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Query Match      99.7%; Score 1814; DB 10; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.6e-152;
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| QY | 2 | ALBONQSTDYEEENENMGITDYSQYELICIKEDVREFAKFLFVFLITIVFVIGLAGNSM | 61 |
| Db | 1 | ALEQNQSTDYEEENMGITDYSQYELICIKEDVREFAKFLFVFLITIVFVIGLAGNSM | 60 |
| QY | 62 | VVAIYAYKKKORTDYIILNLAVADLLFLTPFAVNAVHGVNLCKIMCKITSALYTL | 121 |
| Db | 61 | VVAIYAYKKKORTDYIILNLAAADLLFLTPFAVNAVHGVNLCKIMCKITSALYTL | 120 |
| QY | 122 | NFVSGMGLACISIDRYAAVTKVPSQSGVGPCWIIICECVMMAILLISIPOLVEFYVNDN | 181 |
| Db | 121 | NFVSGMGLACISIDRYAAVTKVPSQSGVGPCWIIICECVMMAILLISIPOLVEFYVNDN | 180 |
| QY | 182 | ARCPIPFPRYIGTSMKALIQMLEICIGFVVPFLMGVCYFTIARTTLKMKPNIKISRLKV | 241 |
| Db | 181 | ARCPIPFPRYIGTSMKALIQMLEICIGFVVPFLMGVCYFTIARTTLKMKPNIKISRLKV | 240 |
| QY | 242 | LLTVAVIEIVTOLYNNIYKFCRAIDIILYSLITSCNMSKRMIDIAIQVYESIALPHSCLNPI | 301 |
| Db | 241 | LLTVAVIEIVTOLYNNIYKFCRAIDIILYSLITSCNMSKRMIDIAIQVYESIALPHSCLNPI | 300 |
| QY | 302 | LYVNGASFKYVMKVAKKYSMKRQNSVEEPFDSGEPLEPSTSI | 350 |
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RESULT 4
US-09-989-442-108
Sequence 108, Application US/09989442
Publication No. US20030013649A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P0208
CURRENT APPLICATION NUMBER: US/09/989,442
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/119,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/217,496
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PRIOR FILING DATE: 2000-08-22
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PRIOR APPLICATION NUMBER: 60/225,267
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PRIOR FILING DATE: 2000-07-07
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PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/241,787
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/246,474
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PRIOR APPLICATION NUMBER: 60/249,210
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/226,681
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/225,759
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/225,213
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/227,182
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/225,214
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/235,836
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/230,438
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/215,135
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 60/225,266
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/249,218
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,208
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,213
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,212
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,207
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,245
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,215
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,264
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,214
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,297
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/232,400
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/231,242
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/232,081
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/232,080
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,414
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,244
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/233,064
PRIOR FILING DATE: 2000-09-14

;; PRIOR APPLICATION NUMBER: 60/233,063
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/232,397
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/232,399
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/232,401
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: 60/241,808
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/241,826
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/241,786
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/241,221
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/246,475
;; PRIOR FILING DATE: 2000-11-08
;; PRIOR APPLICATION NUMBER: 60/231,243
;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: 60/233,065
;; PRIOR FILING DATE: 2000-09-14

Query Match 41.8%; Score 761; DB 9; Length 175;
Best Local Similarity 96.1%; Pred. No. 5, Le-60;
Matches 148; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 197 KALIOMLKLEICIGFVVPFLIMGVCFITARTLKMKNPKIKSRPLKVLTVVIVFIVTOLPY 256
DB 22 ESIDSMLEICIGFVVPFLIMGVCFITERTLKMKNPKIKSRPLKVLTVVIVFIVTOLPY 81
QY 257 NIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVTSIALFHSCNLPILVYFMGASFKNYVMK 316
DB 82 NIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVTSIALFHSCNLPILVYFMGASFKNYVMK 141
QY 317 VAKKYSWRROSVVEFPDSEGPTEPTSTFSI 350
DB 142 VAKKYSWRROSVVEFPDSEGPTEPTSTFSI 175

RESULT 5
US-10-073-865-91
;; Sequence 91, Application US/10073865
;; Publication No. US20030044904A1
;; GENERAL INFORMATION:
;; APPLICANT: Rosen et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;; FILE REFERENCE: PJ20981
;; CURRENT APPLICATION NUMBER: US/10/073,865
;; CURRENT FILING DATE: 2002-02-14
;; Prior Application removed - See file Wrapper or Palm
;; NUMBER OF SEQ ID NOS: 154
;; SOFTWARE: Patentln Ver. 2.0
;; SEQ ID NO 91
;; LENGTH: 175
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (16)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: misc_feature
;; LOCATION: (19)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-073-865-91

Query Match 41.8%; Score 761; DB 9; Length 175;
Best Local Similarity 96.1%; Pred. No. 5, Le-60;
Matches 148; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 197 KALIOMLKLEICIGFVVPFLIMGVCFITARTLKMKNPKIKSRPLKVLTVVIVFIVTOLPY 256
DB 22 ESIDSMLEICIGFVVPFLIMGVCFITERTLKMKNPKIKSRPLKVLTVVIVFIVTOLPY 81

QY 257 NIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVTSIALFHSCNLPILVYFMGASFKNYVMK 316
DB 82 NIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVTSIALFHSCNLPILVYFMGASFKNYVMK 141
QY 317 VAKKYSWRROSVVEFPDSEGPTEPTSTFSI 350
DB 142 VAKKYSWRROSVVEFPDSEGPTEPTSTFSI 175

RESULT 6
US-09-764-853-584
;; Sequence 584, Application US/09764853
;; Patent No. US20020090672A1
;; GENERAL INFORMATION:
;; APPLICANT: Rosen et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;; FILE REFERENCE: PJ206
;; CURRENT APPLICATION NUMBER: US/09/764,853
;; CURRENT FILING DATE: 2001-01-17
;; Prior application data removed - consult PALM or file wrapper
;; NUMBER OF SEQ ID NOS: 939
;; SOFTWARE: Patentln Ver. 2.0
;; SEQ ID NO 584
;; LENGTH: 175
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (16)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: SITE
;; LOCATION: (19)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-853-584

Query Match 41.8%; Score 761; DB 10; Length 175;
Best Local Similarity 96.1%; Pred. No. 5, Le-60;
Matches 148; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 197 KALIOMLKLEICIGFVVPFLIMGVCFITARTLKMKNPKIKSRPLKVLTVVIVFIVTOLPY 256
DB 22 ESIDSMLEICIGFVVPFLIMGVCFITERTLKMKNPKIKSRPLKVLTVVIVFIVTOLPY 81
QY 257 NIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVTSIALFHSCNLPILVYFMGASFKNYVMK 316
DB 82 NIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVTSIALFHSCNLPILVYFMGASFKNYVMK 141
QY 317 VAKKYSWRROSVVEFPDSEGPTEPTSTFSI 350
DB 142 VAKKYSWRROSVVEFPDSEGPTEPTSTFSI 175

RESULT 7
US-09-966-755-2
;; Sequence 2, Application US/09966755
;; Publication No. US20030022238A1
;; GENERAL INFORMATION:
;; APPLICANT: Andrew, David P.
;; APPLICANT: Zabel, Brian A.
;; APPLICANT: Ponath, Paul D.
;; TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
;; IDENTIFYING AGENTS WHICH MODULATE GPR-9-6 FUNCTION
;; FILE REFERENCE: LKS98-16
;; CURRENT APPLICATION NUMBER: US/09/966,755
;; CURRENT FILING DATE: 2001-09-28
;; PRIOR APPLICATION NUMBER: US/09/266,464
;; PRIOR FILING DATE: 1999-03-11
;; NUMBER OF SEQ ID NOS: 7
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 2
;; LENGTH: 357
;; TYPE: PRT

APPLICANT: Zabel, Brian A.
 APPLICANT: Ponath, Paul D.
 TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
 IDENTIFYING MODULATORS OF GPR-9-6 FUNCTION
 FILE REFERENCE: 1855,1064-003
 CURRENT APPLICATION NUMBER: US/10/000,759A
 CURRENT FILING DATE: 2001-10-23
 PRIOR APPLICATION NUMBER: US/09/522,752
 PRIOR FILING DATE: 2000-05-10
 PRIOR APPLICATION NUMBER: US 09/266,464
 PRIOR FILING DATE: 1999-03-11
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: FastSeq for windows Version 4.0
 SEQ ID NO: 2
 LENGTH: 357
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-000-759A-2

Query Match 35.0%; Score 637; DB 12; Length 357;
 Best Local Similarity 36.5%; Pred. No. 1e-48;
 Matches 119; Conservative 74; Mismatches 115; Indels 18; Gaps 4;

10 DYEE-NEKNGTIDYSOVELICKEDEVEFAKFLPVELTIVFVIGLAGNSMVAIAY 68
 4 DYSESTSSMEDYVNFNDYCEKNNVQFASHFLPPLXWLVFVIGLAGNSLVIVVY 63
 69 YKORRTDYYIILAVADLLFTLPEMAVNAHGVGLKIMCKITSAVTLNFSQMO 128
 64 CTWKTMTDFTLNLAIADLLFVTLPEMAIAADQMKFOTMCKVNVNMYKNFYSCLV 123
 129 FLACISIDRVAVATKVPQSGVGKPCW-----IICFCVMAAILISPOLVFTYN 179
 124 LINCISVDRIATAQ-----AKAHMTWREKRLLYSKMVCFTWVLAALCIPEILYSQIK 178
 180 DN---ARCIPIEPRLYGTSMKALIQMLEICIGFVPELIMGVCFITARTLKMPIKIS 236
 179 EESGAICTMVPYDESTKLSAVLTLKGLPELVVACCCYIIITLQAKKSSKH 238
 237 RPLKVLTVVIVYIQLPYNIVKFCRAIDIIYSLTSCNMSKRDIAIOVETALFHS 296
 239 KAKVITVIVLVFVLSQFPYNCILLVOTIDAYAMFISNCVSTNIDICFOVYOTIAFHS 298
 297 CLNPILYFMGASFKNYVAKKYG 322
 299 CLNPILYFVGERERDVLKTLKNG 324

RESULT 11

US-09-852-156-4
 Sequence 4, Application US/09852156
 Patent No. US20020076694A1

GENERAL INFORMATION:

APPLICANT: Littman, Dan R.

Deng, Hongkui
 Untmaz, Derya
 Ramanl, Vineet N.K.

TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS

ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.
 STREET: 411 Hackensack Ave, Continental Plaza, 4th
 Floor

CITY: Hackensack

STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/852,156
 FILING DATE: 09-May-2001
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 1049-1-009NCIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 342 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHEICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: African Green Monkey
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-09-852-156-4

Query Match 31.9%; Score 581; DB 10; Length 342;
 Best Local Similarity 34.2%; Pred. No. 8.2e-44;
 Matches 121; Conservative 71; Mismatches 130; Indels 32; Gaps 8;

12 YEEENMGNTDYSOVELICKEDEVEFAKFLPVELTIVFVIGLAGNSMVAIAYKK 71
 6 HYEDGFNSFNDSSQEE---HDEFLQSKVFLPCMLVLFVCGLVGNSLVLSIFYHK 61
 72 ORTKTDVYIILAVADLLFTLPEMAVNAHGVGLKIMCKITSAVTLNFSQMOFLA 131
 62 LOSLTVLVLPLADLVFVCTLPEMAVAGHEHIEQVCKITLIGITITNFTSMILIT 121
 132 CISIDRYAVATKVP--OSVGKPCW--IICFCVMAAILISPOLVFTYN--NDNARCT 185
 122 CTVDFREFVAVKATKAVNOQAKMTMGKVICLLIWLIVSLVSLPOLIYGVNPLDKLIC 180
 186 PIFPRYLGTSKALIQMLEICIGFVPELIMGVCFITARTLKMPIKISRLPLKLV 245
 181 ---GYHDEISTVLAQTMLGFLPLAMIVCYVIITLLHAGGFQHRSLKTIIFLV 236
 246 VIVEIVQLPYNIVKFCRAIDIIYSLTSCNMSKRDIAIOVETALFSCNPILYVF 305
 237 MAVFLITQTPENLVKLRSTHWEYAMTSFHYT-----IIVETALVLRACLNPILYAF 290
 306 MGASFKNYVAKKYG-----SWROROSVEEFPDSDGPEPTSFST 350
 291 VSLFRKNFMKLVKIDICLPYLGVSQWKSSEDNSK--TFASAHNVEATSMFQL 342

RESULT 12

US-09-852-156-6
 Sequence 6, Application US/09852156
 Patent No. US20020076694A1

GENERAL INFORMATION:

APPLICANT: Littman, Dan R.

Deng, Hongkui
 Untmaz, Derya
 Ramanl, Vineet N.K.

TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS

ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.
 STREET: 411 Hackensack Ave, Continental Plaza, 4th
 Floor

```

      IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USES
      THEREOF
      NUMBER OF SEQUENCES: 20
      CORRESPONDENCE ADDRESS:
      ADDRESSEE: David A. Jackson, Esq.
      STREET: 411 Hackensack Ave, Continental Plaza, 4th
              Floor
      CITY: Hackensack
      STATE: New Jersey
      COUNTRY: USA
      ZIP: 07601
      COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patent In Release #1.0, Version #1.30
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/09/852,156
      FILING DATE: 09-May-2001
      CLASSIFICATION: <Unknown>
      ATTORNEY/AGENT INFORMATION:
      NAME: Jackson Esq., David A.
      REGISTRATION NUMBER: 26,742
      REFERENCE/DOCKET NUMBER: 1049-1-009NCIP
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: 201-487-5800
      TELEFAX: 201-343-1684
      INFORMATION FOR SEQ ID NO: 2:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 342 amino acids
      TYPE: amino acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: protein
      HYPOTHEetical: NO
      ORIGINAL SOURCE:
      ORGANISM: Homo sapiens
      SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-852-156-2
Query Match          30.8%; Score 560; DB 10; Length 342;
Best Local Similarity 33.1%; Pred. No. 5,9e-42;
Matches 117; Conservative 75; Mismatches 130; Indels 32; Gaps 8;
QY    12 YYENEMNGVTYSOYLCTIKEDYREFAKVFLPVLITVFVIGLAGNSMVAIAYYYKK 71
Db     6 YHEDGFSSFNDSQEE---HDFLOFSKYFLPCMYLVFVCGVGNSLVLTISIFYHK 61
QY    72 QRTKTDVYILMLAAVDLLLTFLPRWAVNAVHWGVIKMGKITSAITYLNPFVSQMOLA 131
Db     62 LQSLTDFELVNLPLADLVFCVTLPRMAIYAGIHENVFGGVCKSSLGITVINFTSMILT 121
QY    132 CISIDRYAIVAVRVKS--OSGVGKPCW--IICFCVMMAIIILSIDQLVFTYV--NDMARCI 185
Db     122 CIYDRFLIVVVKAKRANYNQAKRMWGKVTSLLIMVISLSLVSPQIIVGNVFNMDKLIC- 180
QY    186 PIFPRYLTSTSKALIQMLETCIGFYVPPLMGVCYCFITARTLMKMPNIKISRPLKVLTV 245
Db     181 ---GYHDEAISTAVLATOMTLGFFLPILTMIVCVSVTIKTLHLHGFGOKHRHSRLKIPLY 236
QY    246 VIVEFVTDLPINIVKFCGAIDIYSLTSCNMRSKRMDIAIOVESIALFHSCLPNIILVVF 305
Db     237 MAVELLTOMPKNMKFTISTHMEYIAMTSPHY-----INVTEIATLRACLNPDVLYAF 290
QY    306 MGASFKNIVKVVAAKYG-----SWRKROASVEEFPDPSEGTPTSPSI 350
Db     291 VSLFRKRNFMKLVRDGLCLPYLGVSHOWKSSSEDNSK--TFASHNVETATSMFOL 342

```

```

: GENERAL INFORMATION:
: APPLICANT: Briskin, Michael J.
: APPLICANT: Murphy, Kristine E.
: APPLICANT: Wilbanks, Alyson M.
: APPLICANT: Wu, Lijun
: TITLE OF INVENTION: No. US20020090657A1el Antibodies and Ligands for "Bonzo"
: FILE OF INVENTION: Chemokine Receptor
: FILE REFERENCE: 1855.1070-000
: CURRENT APPLICATION NUMBER: US/09/940,063
: CURRENT FILING DATE: 2001-08-27
: PRIOR APPLICATION NUMBER: 09/449,437
: PRIOR FILING DATE: 1999-11-24
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 342
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-940-063-2

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Query Match 30.8%; Score 560; DB 10; Length 342;

Best Local Similarity 33.1%; Pred. No. 5,9e-42;
Matches 117; Conservative 75; Mismatches 130; Indels 32; Gaps 8;

```

QY 12 YEEENENNGTYDYSQELICKEDEYREFAKVFLEPLTYFVIGLAGNSMVAIYAYK 71
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6 YHEYGESSFNDSQEE---HODFLQFSKVFLEPCMYLVFVCGLVGNSLVLVISIFYK 61

QY 72 QRTQTDVYILNLAVADLLFTLPFMAVNAVHGVNLGKIMCKITSAIYTLNPFSGMOFLA 131
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 LQSLTDVFLVNLPLADLVFCTLPFMAVAGIHEWFGQVCKSLGTYITNETSMILIT 121

QY 132 CISIDRYAVATKVS--OSGVGKPCW--IICFCVMAAILLSIPOLVFYV--NDNARCI 185
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 122 CITVDREIVVYKATKAVNOQAKRMWCKVSLIIVISLVSPQIYGVNFDKILIC- 180

QY 186 PIFRRLGTSKALIQMLEICIGFVVPFLMGVCYFTTARTLKMMPNIRKISRPALVIT 245
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 ---GYHDEALSTVLAQMTLGFPLPLTMYICYSVIITKLLHAGGFGKHRSKILITLV 236

QY 246 VIVEIVTOLPYNIVKFCRAIDIIYSLTSCNMSKRMDAIOVTESTIALFSCNIPILYVF 305
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 237 MAVELLTQMPFNLMKFTIRSHWEYAMTSFHYT-----IMVDAIYLAACLNPIYIAR 290

QY 306 MGASFKNVYMKVAKKY-----SWRROROSVEEFPDSGPTPEPTSTESI 350
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 291 VSLKFRKNFMKLVKIDICLPYLGVSQWKSSEDNSK--TFESASHNVATSMFOL 342

```

RESULT 15
US-10-120-394-20
Sequence 20, Application US/10120394
Patent No. US20020160015A1

GENERAL INFORMATION:

APPLICANT: Wells, Timothy N.C.

TITLE OF INVENTION: CHEMOKINE RECEPTOR ABLE TO BIND TO

NUMBER OF SEQUENCES: 20
MCP-1, MIP-1 ALPHA AND/OR RANTES AND ITS USES

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHAYE P.C.

STREET: 1100 NO. US20020160015Alth Glebe Rd. 8th floor

CITY: Arlington

STATE: VA

COUNTRY: USA

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/120,394

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: FILING DATE: 12-Apr-2002
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 09/614,256
: FILING DATE: 12-JUL-2000
: APPLICATION NUMBER: US 08/875,573
: FILING DATE: 31-OCT-1997
: APPLICATION NUMBER: PCT/GB96/00143
: FILING DATE: 24-JAN-1996
: APPLICATION NUMBER: GB 9501683.8
: FILING DATE: 27-JAN-1995
: INFORMATION FOR SEQ ID NO: 20:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 360 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-120-394-20

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Query Match 29.5%; Score 537.5; DB 9; Length 360;

Best Local Similarity 35.8%; Pred. No. 6e-40;
Matches 115; Conservative 63; Mismatches 124; Indels 19; Gaps 6;

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QY 10 DYEEENENNGTYDYSQELICKEDEYREFAKVFLEPLTYFVIGLAGNSMVAIYAYK 69
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 8 DTLDESISYNNYLYESIPKPCCKEIKAFGLPLPYLSLVFVGLGNSVYLVLEKY 67

QY 70 KQRTQTDVYILNLAVADLLFTLPFMAVNAVHGVNLGKIMCKITSAIYTLNPFSGMOF 129
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 68 KRLRSMTDVIYLNLAISDLFLVFSLPFGCYTAADQWVGLGCKMISWYLVGFSGIIF 127

QY 130 LACISIDRYAVATKVS-----PSQGVGKPCWIIICFCVMAAILLSIPOLVF--YTVN 179
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 128 VMLMSIDRYLAIVHAFSLRARTLFTGYV-----ITSLATWSAVAVPASLPGLFSTCYTER 182

QY 180 DNARCIPIFRRLGTSKALIQMLEI-CIGFVVPFLMGVCYFTTARTLKMMPNIRKISRP 238
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 183 NHYCKTKYS--LNSTWVKVLSLEINILGLVPLGIMLFCYSMLIRLQCKCKEKNKA 240

QY 239 LKVLIVVIVFVITOLPYNIVKFCRAIDIIYSLTSCNMSKRMDAIOVTESTIALFHSCL 298
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 241 VKMIRFVAVLFLGFMPYIVIVLETL--VELEVLDCCIFERYLDAIQAETLAVHCL 299

QY 299 NPLIVYFMGASFKNVYMKVAK 319
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 300 NPLIYFELGKFRKYLQLFK 320

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Search completed: March 14, 2003, 16:16:55
Job time : 16 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 16:11:03 ; Search time 32 seconds

(without alignments)
2253.640 Million cell updates/sec

Title: US-09-686-020A-2

Perfect score: 1819

Sequence: 1 MALEONQSTDYEEENEMNG.....VEEPPDSGPTPTSTFSI 350

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SPREMBL_21:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*
16: sp_virus:*
17: sp_bacteriap:*
18: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|-------------------------|
| 1 | 1596 | 87.7 | 350 | 11 Q92413 | Q92413 mus musculus |
| 2 | 1593 | 87.6 | 350 | 11 Q802W9 | Q802W9 mus musculus |
| 3 | 912 | 50.1 | 221 | 11 Q9ESK1 | Q9ESK1 rat mus musculus |
| 4 | 643 | 35.3 | 369 | 4 Q9U006 | Q9U006 homo sapien |
| 5 | 611 | 33.6 | 367 | 11 Q9R1V0 | Q9R1V0 mus musculus |
| 6 | 586.5 | 32.2 | 368 | 13 Q42444 | Q42444 oncorhynch |
| 7 | 578 | 31.8 | 343 | 6 Q9N020 | Q9N020 cercocebus |
| 8 | 566.5 | 31.1 | 351 | 11 Q9E016 | Q9E016 mus musculus |
| 9 | 566 | 31.1 | 343 | 6 Q9BDS6 | Q9BDS6 macaca fasc |
| 10 | 561.5 | 30.9 | 351 | 11 Q9ERH5 | Q9ERH5 mus musculus |
| 11 | 560 | 30.8 | 342 | 4 Q9HCAS | Q9HCAS homo sapien |
| 12 | 559 | 30.7 | 342 | 6 Q9TV16 | Q9TV16 pan troglod |
| 13 | 544 | 29.9 | 358 | 13 Q9PUA0 | Q9PUA0 acipenser r |
| 14 | 534.5 | 29.4 | 360 | 11 Q912H4 | Q912H4 rattus norv |
| 15 | 529 | 29.1 | 361 | 11 Q9VHP3 | Q9VHP3 cavia porce |
| 16 | 520.5 | 28.6 | 358 | 13 Q9YGC3 | Q9YGC3 xenopus lae |

| | | | | | |
|----|-------|------|-----|-----------|--------------------|
| 17 | 516 | 28.4 | 355 | 11 Q9JLX8 | Q9JLX8 rattus norv |
| 18 | 507.5 | 27.9 | 347 | 6 Q9MZM1 | Q9MZM1 eulemur mac |
| 19 | 507 | 27.9 | 357 | 13 Q42445 | Q42445 oncorhynch |
| 20 | 506.5 | 27.8 | 347 | 6 Q9MZM7 | Q9MZM7 callimico g |
| 21 | 506.5 | 27.8 | 347 | 6 Q9MZM6 | Q9MZM6 callimico g |
| 22 | 503.5 | 27.7 | 347 | 6 Q9MZM0 | Q9MZM0 alouatta se |
| 23 | 503.5 | 27.7 | 352 | 6 Q9V444 | Q9V444 cercopithec |
| 24 | 502.5 | 27.6 | 347 | 6 Q9V444 | Q9V444 cercopithec |
| 25 | 502.5 | 27.6 | 347 | 6 Q9V444 | Q9V444 cercopithec |
| 26 | 502.5 | 27.6 | 347 | 6 Q9V444 | Q9V444 cercopithec |
| 27 | 502.5 | 27.6 | 347 | 6 Q9V444 | Q9V444 cercopithec |
| 28 | 500.5 | 27.5 | 347 | 6 Q9V444 | Q9V444 cercopithec |
| 29 | 500.5 | 27.5 | 347 | 6 Q9V444 | Q9V444 cercopithec |
| 30 | 500.5 | 27.5 | 347 | 6 Q9V444 | Q9V444 cercopithec |
| 31 | 500.5 | 27.5 | 347 | 6 Q9V444 | Q9V444 cercopithec |
| 32 | 500.5 | 27.5 | 347 | 6 Q9V444 | Q9V444 cercopithec |
| 33 | 500.5 | 27.5 | 347 | 6 Q9V444 | Q9V444 cercopithec |
| 34 | 499.5 | 27.5 | 339 | 6 Q9V444 | Q9V444 cercopithec |
| 35 | 499.5 | 27.5 | 339 | 6 Q9V444 | Q9V444 cercopithec |
| 36 | 499.5 | 27.5 | 347 | 6 Q9V444 | Q9V444 cercopithec |
| 37 | 499.5 | 27.5 | 347 | 6 Q9V444 | Q9V444 cercopithec |
| 38 | 499.5 | 27.5 | 347 | 6 Q9V444 | Q9V444 cercopithec |
| 39 | 499.5 | 27.5 | 347 | 6 Q9V444 | Q9V444 cercopithec |
| 40 | 499.5 | 27.5 | 347 | 6 Q9V444 | Q9V444 cercopithec |
| 41 | 499.5 | 27.5 | 347 | 6 Q9V444 | Q9V444 cercopithec |
| 42 | 499.5 | 27.5 | 347 | 6 Q9V444 | Q9V444 cercopithec |
| 43 | 499.5 | 27.5 | 347 | 6 Q9V444 | Q9V444 cercopithec |
| 44 | 499.5 | 27.5 | 347 | 6 Q9V444 | Q9V444 cercopithec |
| 45 | 499.5 | 27.5 | 347 | 6 Q9V444 | Q9V444 cercopithec |

ALIGNMENTS

RESULT 1

| | | | | |
|----|---|--------------|------|---------|
| ID | Q92413 | PRELIMINARY: | PRT: | 350 AA. |
| AC | Q92413 | Q92413 | | |
| DT | 01-DEC-2001 (TREMBLrel. 19, Created) | | | |
| DT | 01-DEC-2001 (TREMBLrel. 19, Last sequence update) | | | |
| DT | 01-JUN-2002 (TREMBLrel. 21, Last annotation update) | | | |
| DE | Chemokine receptor CCR11. | | | |
| OS | Mus musculus (Mouse). | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. | | | |
| OX | NCBI_TaxID=10090; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=BALE/C; | | | |
| RX | MEDLINE=20519697; PubMed=11063828; | | | |
| RA | Dorf M.E., Berman M.A., Tanabe S., Heesen M., Luo Y.; | | | |
| RT | "Astrocytes express functional chemokine receptors."; | | | |
| RL | J. Neuroimmunol. 111:109-121(2000). | | | |
| DR | EMBL: AF306532; AAK81712.1; | | | |
| DR | InterPro: IPR000276; GPCR_Kinopsn. | | | |
| DR | PIfam: PF00001; 7tm_1; 1. | | | |
| DR | PRINTS: PRO1557; CHEMOKINER10. | | | |
| DR | PRINTS: PRO1558; CHEMOKINER11. | | | |
| DR | PRINTS: PRO1559; DUFFYANTIGEN. | | | |
| DR | PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; UNKNOWN_1. | | | |
| DR | PROSITE: PS00262; G_PROTEIN_RECPT_FL_2; 1. | | | |
| KW | Receptor. | | | |
| SQ | SEQUENCE 350 AA: 39530 MW; C5F7D9DC949CECCF CRC64; | | | |

Query Match 87.7%; Score 1596; DB 11; Length 350;

Best local Similarity 85.4%; Pred. No. 4e-137;

Matches 299; Conservative 26; Mismatches 25; Indels 0; Gaps 0;

| | | |
|----|----|--|
| QY | 1 | MALEONQSTDYEEENEMNGTYDYSEYELICKEDYREFAKVFLPVLTIVFVIGLAGNS 60 |
| DB | 1 | MALEONQSTDYEEENEMNGTYDYSEYELICKEDYREFAKVFLPVLTIVFVIGLAGNS 60 |
| QY | 61 | MVAIAIYAIYKKKTKTDYIILNLAVALDLLLFLPPRAVNAVHGWLGKIMCKITSALYT 120 |

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Db 61 VVAIVAYAKKQRTKTDVYIINLAVALDLLLITLPMVAVNAVHGMILGKMKCKVTSALYT 120
      :|||||
Qy 121 LNFSVGMQFLACISIDRYVAATKVPSSGVGKPCMIICFCVMAAILLSIPOLVEFYVND 180
      :|||||
Db 121 VNFSVGMQFLACISIDRYVAATKVPSSGVGKPCMIICFCVMAAILLSIPOLVEFYVND 180
      :|||||
Qy 181 NARCIPIFPRLYGTSMKALIQMLEICIGFVVPFLIMGVCFYITARTLMPKPNIKISRPLK 240
      :|||||
Db 181 NARCIPIFPRLYGTSMKALIQMLEICIGFVVPFLIMGVCFYITARTLMPKPNIKISRPLR 240
      :|||||
Qy 241 VLVTVVVFYITQLPYNNVVKFCRAIDIIYLSITSCNMSKRMDAIQVTESTIALFHSCLP 300
      :|||||
Db 241 VLVTVVVFYITQLPYNNVVKFCRAIDIIYLSITSCNMSKRMDAIQVTESTIALFHSCLP 300
      :|||||
Qy 301 ILVYFMGASFKNYIMKAKKYSNRROKROSVSEEPFDESGTEPTSTFSFI 350
      :|||||
Db 301 ILVYFMGASFKNYIMKAKKYSNRROKROSVSEEPFDESGTEPTSTFSFTI 350
      :|||||

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RESULT 2

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Q08QZM9 PRELIMINARY; PRT; 350 AA.
ID 08QZM9
AC 08QZM9
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE Chemokine receptor CCX CKR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA "Townson J.R., Nibbs R.J.: CCX CKR, a receptor for the lymphocyte-
  attracting chemokines TECK (CCL25), SLC (CCL21) and MIP-3beta (CCL19):
  RT characterization of mouse CCX CKR, a receptor for the lymphocyte-
  attracting chemokines TECK (CCL25), SLC (CCL21) and MIP-3beta (CCL19):
  RT comparison to human CCX CKR."
  RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
  DR EMBL: AY072796; AAL68400.1; -.
  DR EMBL: AY072938; AAL68962.1; -.
  KW Receptor.
  SQ SEQUENCE 350 AA; 39544 MW; D017CC29749CECD5 CRC64;

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Query Match 87.6%; Score 1593; DB 11; Length 350;
Best local Similarity 85.1%; Pred. No. 7.5e-137;
Matches 298; Conservative 27; Mismatches 25; Indels 0; Gaps 0;

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```

Qy 1 MALEONOSTDYIEENENGTYYISQYELICIKEDVREPAKVLPLVTVYVIGLAGNS 60
      :|||||
Db 1 MALELNQSAEYEEENENYTHDSQYEVICIKEDVROPAKVLPAFVAFVGLAGNS 60
      :|||||
Qy 61 MVVAIVAYAKKQRTKTDVYIINLAVALDLLLITLPMVAVNAVHGMILGKMKCKVTSALYT 120
      :|||||
Db 61 VVAIVAYAKKQRTKTDVYIINLAVALDLLLITLPMVAVNAVHGMILGKMKCKVTSALYT 120
      :|||||
Qy 121 LNFSVGMQFLACISIDRYVAATKVPSSGVGKPCMIICFCVMAAILLSIPOLVEFYVND 180
      :|||||
Db 121 VNFSVGMQFLACISIDRYVAATKVPSSGVGKPCMIICFCVMAAILLSIPOLVEFYVND 180
      :|||||
Qy 181 NARCIPIFPRLYGTSMKALIQMLEICIGFVVPFLIMGVCFYITARTLMPKPNIKISRPLK 240
      :|||||
Db 181 NARCIPIFPRLYGTSMKALIQMLEICIGFVVPFLIMGVCFYITARTLMPKPNIKISRPLR 240
      :|||||
Qy 241 VLVTVVVFYITQLPYNNVVKFCRAIDIIYLSITSCNMSKRMDAIQVTESTIALFHSCLP 300
      :|||||
Db 241 VLVTVVVFYITQLPYNNVVKFCRAIDIIYLSITSCNMSKRMDAIQVTESTIALFHSCLP 300
      :|||||
Qy 301 ILVYFMGASFKNYIMKAKKYSNRROKROSVSEEPFDESGTEPTSTFSFI 350
      :|||||
Db 301 ILVYFMGASFKNYIMKAKKYSNRROKROSVSEEPFDESGTEPTSTFSFTI 350
      :|||||

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RESULT 3

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Q09ESK1 PRELIMINARY; PRT; 221 AA.
ID 09ESK1
AC 09ESK1
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE Putative G-protein coupled receptor GPCR4 (Fragment).
GN GPCR4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HARLAN SPRAGUE-DAWLEY;
RA Carroll S.L., Miller M.L., Benedict-Hamilton H.M.:
  RT "Identification and characterization of novel G-protein coupled
  RT receptors expressed in regenerating peripheral nerve."
  RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
  DR EMBL: AF090348; AAG24470.1; -.
  DR InterPro: IPR000276; GPCR_Rhodpsn.
  DR Pfam: PF00001; 7tm.1; 1.
  DR PRINTS: PRO1557; CHEMOKINER10.
  DR PRINTS: PRO0237; GPCR_RHODOPSIN.
  DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
  DR PROSITE: PS50262; G_PROTEIN_RECP_F1_2; 1.
  KW Receptor.
  FT NON_TER 1 1
  FT NON_TER 221 221
  SQ SEQUENCE 221 AA; 24342 MW; 5622DD607378A6C CRC64;

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Query Match 50.1%; Score 912; DB 11; Length 221;
Best local Similarity 83.3%; Pred. No. 4e-75;
Matches 169; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

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Qy 96 FMAVNAVHGMILGKIMCKITSLALYLVNFSVGMQFLACISIDRYVAATKVPSSGVGKPCW 155
      :|||||
Db 19 FMAVNAVHGMILGKIMCKITSLALYLVNFSVGMQFLACISIDRYVAATKVPSSGVGKPCW 78
      :|||||
Qy 156 IICFCVMAAILLSIPOLVEFYVNDNARCIPIFPRLYGTSMKALIQMLEICIGFVVPFLI 215
      :|||||
Db 79 IICCCVMAAILLSIPOLVEFYVNDNARCIPIFPRLYGTSMKALIQMLEICIGFVVPFLI 138
      :|||||
Qy 216 MGVCYITARTLMPKPNIKISRPLKVLTVVVFYITQLPYNNVVKFCRAIDIIYLSITSC 275
      :|||||
Db 139 MGVCYITARTLMPKPNIKISRPLKVLTVVVFYITQLPYNNVVKFCRAIDIIYLSITSC 198
      :|||||
Qy 276 NMSKRMDAIQVTESTIALFHSC 298
      :|||||
Db 199 NMSKRMDAIQVTESTIALFHSC 221
      :|||||

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RESULT 4

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Q09Q006 PRELIMINARY; PRT; 369 AA.
ID 09Q006
AC 09Q006
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Chemokine receptor CCR9 (CC chemokine receptor 9A).
GN CCR9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99248139; PubMed=10229797;
RA Zaballos A., Gutierrez J., Varona R., Ardavin C., Marquez G.:
  RT "Identification of the orphan chemokine receptor GPR-9-6 as CCR9, the
  RT receptor for the chemokine TECK."

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Db 17 YDSSFTFTVEEDVDNFMCDKSAVRAFRGOYEPLLYWVILGGLNLTVMVYILHFR 76
Qy 71 KO-RRTDYVILNLAVALDLLFTLPFWANAVNAHGVGLKIMCKITSAIYLTLEFVSGMOF 129
Db 77 ORLKTMDIYILNLAVALDFLGLTLPMAVEANQMSGDLGCKATSAFYKINFEFSSMLL 136
Qy 130 LACISIDRYVAVTKVPSOSGVK-P-----CWILCFVWMAAILLSIPOLVFYVND--NA 182
Db 137 LVCISIDRYVAVTKVPSOSGVK-P-----CWILCFVWMAAILLSIPOLVFYVND--NA 182
Qy 183 RCIPFPRYLGTSMKALLIOMLEICIGFVVPFLIMGVCFYFARTLTKMKPNKISRLPKVL 242
Db 197 YCTVYVWMSNQRRTKIVLVGLDLCIGFCLPLVAVFCYAGIIRTLTKRSQYKHALKVI 256
Qy 243 LTVVIVFVLTOLPYNIVKFCRAIDIIYSLTSCNMSKRMIDIAIOVTSIALFHSCLNPL 302
Db 257 LVVAVFVLSQLPYNSVLYMEATQANSTQDCSAKRFNVSVOLKSLAVTHACLNPFL 316
Qy 303 YVFMGASFKNYVMKAKKYGSW 324
Db 317 YVFGVFRRLDLKLRLYHGW 338

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RESULT 7

```

Q9N020 PRELIMINARY; PRT; 343 AA.
ID 09N020:
AC 09N020:
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE STRL33.
OC Cercopithecus torquatus alyus (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20261727; Pubmed=10799581;
RA Pohlmann S., Lee B., Meister S., Krumbiegel M., Leslie G., Doms R.W.,
RA Kirchhoff F.,
RT "Simian immunodeficiency virus utilizes human and sooty mangabey but
RT not thes macaque STRL33 for efficient entry.",
RL J. Virol. 74:5075-5082(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Pohlmann S., Lee B., Meister S., Krumbiegel M., Leslie G., Doms R.W.,
RA Kirchhoff F.,
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF237559; AAF68392.1;
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
SQ SEQUENCE 343 AA; 39589 MW; A75B7A0751C13455 CRC64;

```

Query Match 31.8%; Score 578; DB 6; Length 343;
 Best Local Similarity 33.7%; Pred. No. 1.5e-44;
 Matches 120; Conservative 73; Mismatches 131; Indels 32; Gaps 8;

```

Qy 10 DYVEENENMGTYDYSOYELICIKEDVREFAKVFLPVFLTYFVIGLAGNSMVAIYAY 69
Db 5 DRYEDEFENFNSDSQKE-----HDFLOFSKVFPLPCMKLVVFCGLVNSLVYISITY 60
Qy 70 KKRRTDYVILNLAVALDLLFTLPFWANAVNAHGVGLKIMCKITSAIYLTLEFVSGMOF 129
Db 61 HKQSLDVLDELNLPLADLVFVCTLPFWAVAGIHEWIFEQVCKTLLGVTINFTSMLI 120
Qy 130 LACISIDRYVAVTKVPS--QSGVGKPCW--IICFCVWMAAILLSIPOLVFYV--NDNAR 183
Db 121 LNCITVDRIVVYKATKAVNQAKRTWGVICLLIWTISLVSIPQIITGVNFMCLKI 180

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Qy 184 CIPFPRYLGTSMKALLIOMLEICIGFVVPFLIMGVCFYFARTLTKMKPNKISRLPKVL 243
Db 181 C-----RYHDEISTVLAOTMLTGFLPLTMTVICYSVILKILHLAGGQKRSKIIF 235
Qy 244 TVVIVFVLTOLPYNIVKFCRAIDIIYSLTSCNMSKRMIDIAIOVTSIALFHSCLNPL 303
Db 236 LVVAVFVLSQLPYNSVLYMEATQANSTQDCSAKRFNVSVOLKSLAVTHACLNPVL 289
Qy 304 VFMGASFKNYVMKAKKYG-----SKRORQSVEEPPDESGPTPTSTFSI 350
Db 290 AFVSLAFKRNKMKLVXDIGCLPYLGVSQWKSSEDSNK--TESASHNVATSMFOL 343

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RESULT 8

```

Q9E016 PRELIMINARY; PRT; 351 AA.
ID 09E016:
AC 09E016:
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Chemokine receptor CXCR6.
GN CXCR6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6.
RX MEDLINE=21177382; Pubmed=11017100;
RA Madhoubian M., David A., Engel S., Ryan J.E., Cyster J.G.;
RT "A transmembrane CXC chemokine is a ligand for HIV-coreceptor Bonzo.",
RL Nat. Immunol. 1:298-304(2000).
DR EMBL; AF301018; AAG34367.1;
DR MGD; MGI:1934582; CXCR6.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 351 AA; 40468 MW; 5658788372B4C65A CRC64;

```

Query Match 31.1%; Score 566.5; DB 11; Length 351;
 Best Local Similarity 35.4%; Pred. No. 1.7e-43;
 Matches 127; Conservative 70; Mismatches 125; Indels 37; Gaps 10;

```

Qy 10 DYVEEN--ENMGTYDYSOYELICIKEDV--EFAKVFPLPVFLTYFVIGLAGNSMVAI 65
Db 12 DGHYGDFTWLFENSSDNSQ-----ENKRFLKKEVFLPCVYLVVVFGLGNSLVLI 64
Qy 66 YAYYKORTKTDVYILNLAVALDLLFTLPFWANAVNAHGVGLKIMCKITSAIYLTLEFVS 125
Db 65 YIFVYKLTLLDVLNLPLADLVFVCTLPFWAAAGTEWYFVGVCKTLLRGMTNMFYV 124
Qy 126 GQGLFACISIDRYAV--TVPSQSGVGKPCW--IICFCVWMAAILLSIPOLVFYVND 180
Db 125 SMLTLTCTVDRFVIVVQATKAFNRQAKM--IMQVILCLILVSVLVSIPQIITGVND 183
Qy 181 NARCIPIPRYLGTSMKALLIOMLEICIGFVVPFLIMGVCFYFARTLTKMKPNKISRLPK 240
Db 184 IDKL--CQYHSEISTVLAOTMLTGFLPLTMTICVSGIITKLLHARNFCQKHSKL 240
Qy 241 VLVVIVFVLTOLPYNIVKFCRAIDIIYSLTSCNMSKRMIDIAIOVTSIALFHSCLNPL 300
Db 241 IIFLVAVFLLTQFPNLMILIOSTMEYITIS-----FKAIYVTEIAIVFRACLNP 294
Qy 301 ILVFMGASFKNYVMKAKKYG-----SMRORQSVEEPPDESGPTPTSTFSI 350
Db 295 VLVAFVGLKFRKNWKLMDKIDGLSHLGVSQWKSSEDSK--TCSASHNVETTSMFOL 351

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RESULT 9
Q9BDS6 PRELIMINARY; PRT; 343 AA.
ID Q9BDS6 PRELIMINARY; PRT; 343 AA.
AC Q9BDS6 PRELIMINARY; PRT; 343 AA.
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Orphan seven transmembrane receptor STRL33.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21134756; PubMed=11242524;
RA Wade-Evans A.M., Russell J., Jenkins A., Javan C.;
RT "Cloning and sequencing of cynomolgus macaque ccr3, gp125, and strl33:
RT potential coreceptors for HIV type 1, HIV type 2, and SIV."
RL AIDS Res. Hum. Retroviruses 17:371-375(2001).
DR EMBL: AF291671; AAK25742.1;
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.
DR PROSITE: PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW Receptor; Transmembrane
SQ SEQUENCE 343 AA; 39472 MW; 0961328948E7784 CRC64;

Query Match 31.1%; Score 566; DB 6; Length 343;
Best Local Similarity 33.1%; Pred. No. 1.8e-43;
Matches 118; Conservative 73; Mismatches 133; Indels 32; Gaps 8;

QY 10 DYYEENNGTYYDSQYELICIKEDVREFAKVFELPVLITVFIYGLAGNSMVAIYAY 69
DB 5 DHYEDGDFLNSDSQSB---HODFLOQFRKVFPCMYLVFVCGVLGNSLVLVISIFY 60
QY 70 KQRTKQRTDYIYNLAVADLLFTLPFMAVNAVHGVNLGKIMCKITSALTYLNFVSQMF 129
DB 61 HKQLSLTDVFLNPLADLVFVCTLPFMAVNAVHGVNLGKIMCKITSALTYLNFVSQMF 120
QY 130 IACISIDRYAVATKVP--QSGVGKPCW--IICFCVMAAILSTIPOLVFYTV--NDNAR 183
DB 121 LITCITVDRIYVVKATKAYNOOAKRMGTGKVICLIIVIVISLVSIPQIYGNVFLDKLI 180
QY 184 CIPFPRPLGTSMKALLIOMLEICIGFVYVPELMGVCYFIFARTLMKMNKISRPKVL 243
DB 181 C---GHNDEISTVVLATQMTLGFPLAMIVCYVILTKTLHAGGFQKHSKLITF 235
QY 244 TVIVFIYVTVLPYINIVKFCRAIDILYSLTSCNMSKRMIDIAIOVETSIALFHSCLNP 303
DB 236 LVMAVFLITQTFPFLNKLIRSTRMEYAMTSFHT-----IIVETALIVLACINPVL 289
QY 304 VEMGASFKNYVYKAKYK-----SWRRQSVYEEPPDSGTEPTSTFSI 350
DB 290 AVFSLSKFRKFNKLVKIDIGCLPYLGVSQWKSSEDNSK--TFSASHNVEATSMFOL 343

RESULT 10
Q9ERH5 PRELIMINARY; PRT; 351 AA.
ID Q9ERH5 PRELIMINARY; PRT; 351 AA.
AC Q9ERH5 PRELIMINARY; PRT; 351 AA.
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Putative chemokine receptor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-C57BL/6; TISSUE=SPLEEN;
RA Sato H., Taniguchi M.;
RT "Molecular cloning of a putative chemokine receptor preferentially
RT expressed in mouse lymphocytes."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF305709; AAG31284.1;
DR MGI: 1934582; Cxcr6.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.
DR PROSITE: PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW Receptor.
SQ SEQUENCE 351 AA; 40511 MW; B00E3134D2B4DIED CRC64;

Query Match 30.9%; Score 561.5; DB 11; Length 351;
Best Local Similarity 35.4%; Pred. No. 4.7e-43;
Matches 127; Conservative 69; Mismatches 126; Indels 37; Gaps 10;

QY 10 DYYEEN--EMNGTYDSQYELICIKEDV--EFAKVFELPVLITVFIYGLAGNSMVAI 65
DB 12 DGHYEGDFLNSDSQSB---ENKRELFKEVFLPCVYLVFVFGGLGNSLVLI 64
QY 66 YAYKKQRTDYIYNLAVADLLFTLPFMAVNAVHGVNLGKIMCKITSALTYLNFVS 125
DB 65 YIFQKRTLDVFLNPLADLVFVCTLPFMAVNAVHGVNLGKIMCKITSALTYLNFVS 124
QY 126 GMOFLACISIDRYAV--TRVPSQSGKPCW--IICFCVMAAILSTIPOLVFYTVND 180
DB 125 SMLITCITVDRIYVVKATKAYNOOAKRMGTGKVICLIIVIVISLVSIPQIYGNV 183
QY 181 NARCIPIPRPLGTSMKALLIOMLEICIGFVYVPELMGVCYFIFARTLMKMNKISRP 240
DB 184 IDKLT---COYHSEISTVVLATQMTLGFPLAMIVCYVILTKTLHAGGFQKHSKLIT 240
QY 241 VLLTVFIYVTVLPYINIVKFCRAIDILYSLTSCNMSKRMIDIAIOVETSIALFHSCLNP 300
DB 241 IIFLVAVFLITQTFPFLNKLIRSTRMEYAMTSFHT-----FKAIIVETALIVLACINP 294
QY 301 ILVYMGASFKNYVYKAKYK-----SWRRQSVYEEPPDSGTEPTSTFSI 350
DB 295 VLVAVFLGKFRKFNKLVKIDIGCLSHLVSSQWKSSEDNSK--TCSASHNVEATSMFOL 351

RESULT 11
Q9HCAS PRELIMINARY; PRT; 342 AA.
ID Q9HCAS PRELIMINARY; PRT; 342 AA.
AC Q9HCAS PRELIMINARY; PRT; 342 AA.
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Mutant G protein-coupled receptor STRL33.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97311099; PubMed=9166430;
RA Liao F., Alkhatib G., Peden K.W., Sharma G., Berger E.A., Farber J.M.;
RT "STRL33, A novel chemokine receptor-like protein, functions as a
RT fusion cofactor for both macrophage-tropic and T cell line-tropic HIV-
RT 1."
RL J. Exp. Med. 185:2015-2023(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA An P., Winkler C., O'Brien S.J.;
RT "The influence of a STRL33 mutant on the course of HIV-1 infection."
RT Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.

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QY 182 A---RCIPFPRLYGTSMKALIQMLEICIGFVVPFLIMGVCFYFARTLTK-MPNIKISR 237
 ID 0912H4 PRELIMINARY; PRT; 360 AA.
 AC 0912H4;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE C-C-chemokine receptor 4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SMPAIN-LEM;
 RA Garcia G.E., Chen S., Xia Y., Harrison J., Wilson C.B., Johnson R.J.,
 RA Bacon K.B., Feng L.;
 RT "Mononuclear cell-infiltrate inhibition by blocking macrophage-derived
 RT chemokine results in attenuation of developing crescentic
 RT glomerulonephritis."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF432872; AAL30398.1;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR01559; DDFEYANTIGEN.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 360 AA; 41218 MW; 50956CD299E1F8B CRC64;

RESULT 14
 Query Match 29.4%; Score 534.5; DB 11; Length 360;
 Best Local Similarity 34.7%; Pred. No. 1.4e-40;
 Matches 113; Conservative 67; Mismatches 127; Indels 19; Gaps 6;

QY 3 LEQNSDYEEENMGTYDYSOYELICIKEDYREFAKVPFLPVLTIVYIGLAGNSMY 62
 ID 0912H4 PRELIMINARY; PRT; 360 AA.
 AC 0912H4;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE C-C-chemokine receptor 4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SMPAIN-LEM;
 RA Garcia G.E., Chen S., Xia Y., Harrison J., Wilson C.B., Johnson R.J.,
 RA Bacon K.B., Feng L.;
 RT "Mononuclear cell-infiltrate inhibition by blocking macrophage-derived
 RT chemokine results in attenuation of developing crescentic
 RT glomerulonephritis."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF432872; AAL30398.1;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR01559; DDFEYANTIGEN.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 360 AA; 41218 MW; 50956CD299E1F8B CRC64;

RESULT 15
 ID 08VHP3 PRELIMINARY; PRT; 361 AA.
 AC 08VHP3;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE CC-chemokine receptor 4.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jopling L.A., Sabroe I., Andrew D.P., Mitchell T.J., Li Y.,
 RA Hodge M.R., Williams T.J., Pease J.E.;
 RT "The identification, characterization and distribution of guinea pig
 RT CCR4 and epitope mapping of a blocking antibody."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF431971; AAL57488.1;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodpsn.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 361 AA; 41064 MW; 9304E897D4FD6839 CRC64;

Query Match 29.1%; Score 529; DB 11; Length 361;
 Best Local Similarity 36.0%; Pred. No. 4.4e-40;
 Matches 118; Conservative 66; Mismatches 104; Indels 40; Gaps 10;

Search completed: March 14, 2003, 16:13:21
 Job time : 37 secs

QY 9 TDYVEENMGTYDYSOYELICIKEDYREFAKVPFLPVLTIVYIGLAGNSMYA1YAY 68
 ID 08VHP3 PRELIMINARY; PRT; 361 AA.
 AC 08VHP3;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE CC-chemokine receptor 4.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jopling L.A., Sabroe I., Andrew D.P., Mitchell T.J., Li Y.,
 RA Hodge M.R., Williams T.J., Pease J.E.;
 RT "The identification, characterization and distribution of guinea pig
 RT CCR4 and epitope mapping of a blocking antibody."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF431971; AAL57488.1;
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodpsn.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 361 AA; 41064 MW; 9304E897D4FD6839 CRC64;

